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           17 SEA FILE=HUAPLIN ABB=IN IL: DR L:4 OR L:7
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L., 5
            3 SEA FILE=HUAPLUU ABB=ON 121 AND DELTA(W (12 OR 15)
           19 SEA FILE=HUAPLUN ABB=ON 116 DE L22 OR L23
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L24 ANSWER 1 OF 19 HCAPLUS CUPYRIGHT 1997 AMS
KATHLEEN FULLER, BT/LIBRARY 308-4290

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1997:628484
             - Document No. 127:316834 Rapid and transient induction of a
     parskey microsomal .DELTA.12 fatty
     acid desaturase mRNA by fungal elimitor. Hirach,
     Christoph; Hahlbrook, Klaus; Semssich, Imre E. (Max-Planck-Institut
     fur Suchtungsforschung, Abteilung Bioch-mie, Cologne, D-50829,
     Germany). Plant Engsich., 115(1), 283-130 (English) 1997. CODEN:
     FLPHAY. 188N: 008: -0889. Publisher: American Society of Plant
     Physiplogists.
    Treatment of cultured pursley (Petroselinum crispum) cells with a
AΒ
     structurally defined paptide elicitor (Pap25) of fungal origin has
    previously been shown to cause rapid and large changes in the levels
     of various desatd. fatty acids. Two
    distinct parsley oMMAs were isolated sharing high sequence
     simularity with miorosomal .omega.-6 fatty acid
     desaturases (FADs). One of them was functionally identified
     as a .DELTA.12 FAD by empression in the yeast
     Saddranomydes perevisiae. Two diencid fatty adids, hexadedadiencid
     and limoleic, which were not detectable in control cells, together
     constituted up to 1.. of the total fatty holds in the transformed
     yeast bells. .DELTA.12 FAD mRNA abbumulated
     rapidly and transiently in elicitor-treated parsley cells,
     protoplasts, and leaves. These and previous results indicate that
     fatty acid desath. is an important early
     component of the conglex defense response of parsley to attempted
     fungal infection.
CC
     11-1 (Flant Bitchem:stry)
    Section dross-reference(s): 3, 7
     paraley fatty acid desaturase fungal
     elimiter; infection fungi parsley fatty acid
     desaturase; Pepli elicitor fatty acid
     desaturase paraley
     Ehytralexin-eliditing hormones
     FL: PAC (Biological activity or effector, except adverse); BICL
     (Backlewical study)
        (Rep 25; rapid and transient induction of a parsley microsomal
      .DELTA.12 fatty acid
      desaturase mENA by fungal elicitor)
    cDML sequences
        fice parsley microschal .DELTA.12
      fatty acid desaturase responsive to
        fungal elimitor,
     Protein seguences
        Fif paraley microsconal .DELTA.12
      fatty acid desaturase responsive to
        fundal elicitor:
ΙT
     Earnley (Fetroselinum crispum)
        (rapid and transient induction of a parsley microsomal
      .DELTA.12 fatty acid
      desaturase mENA by fungal elicitor)
     197594-14-2 197594-15-3
IΤ
     FL: FFM (Biological process); PRP (Properties); BIOL (Biological
     study); PROC (Epoches)
        commind acid sequence; rapid and transient induction of a parsley
        miprosemal .DELTA.12 fatty
     acid desaturase mEMA by fungal elicitor)
180442-90-4, GenBank U70748 197698-97-8
     FL: BPH (Piclogical process); PEP (Properties); BIOL (Biological
     study); PEOC (Process)
        indulectide sequence; rapid and transient induction of a parsley
       nuclosomal .DELTA.12 fatty
     acid desaturase mENA ky fungal elicitor)
     64618-41-9, Fatty acid .DELTA.
     12-desaturase
     KL: BPE (Biological process); PEP (Properties); BIOL (Biological
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study); PROC (Process)
        (rapid and transient induction of a parsley microsomal
      .DELTA.12 fatty acid
      desaturase mPMA by fungal elicitor)
     67826-35-4, Fatty acid .omega.-1
ΙT
     desaturase
     EL: BST (Biblogical Atudy, unclassified); PRP (Properties); BIOL
     (Biological study)
        (rapid and transient industion of a parsley misrosomal
      .DELTA.12 fatty acid
      desaturase mEMA by fungal elicitor:
L24 ANSWER 2 OF 19 HCAPLUS COPYRIGHT 1997 ACS
             Document No. 127:25:44: The pleate desaturase product of
1997:610711
     the FALC-N gene of hazel and its uses. Dani, Maria; Catello, Sergio
     (Spremartoe S.A., Belg.; Ferrero S.P.A.). Eur. Pat. Appl. EP 794250
     A1 970910, 29 pp. DEŜIGNATED STATES: E: BE, ES, FR, GB, IT, NL. English). CODEN: EPXXDW. APPLICATION: EP 97-103098 970226.
     ERIORITY: OH 9--580 960804.
AΒ
     The FADD-N gene of hazel (Corylus swellang L.) coming for the .
     DELTA.12 desaturuse enzyme of the microsomal
     fraction is bloned and characterized for use as a probe for the
     isplation of other plant desaturase genes. The gene can also be
     used to alter the desaturase levels and consequently the
     fatty-acid compn. of a plant. Enobes denoved from
     the Arabidopsis .DELTA.12 desaturase gene were
     used to sureer a hazel cDNA bank from ripo Corylus avellana cv. San
     Giovanni in .lambda.CAPII.
    10M CLLN 15-5:
FGC C12N015-82; C12N609-02; C12N605-10; C12Q001-68
TC
ICA ACTHODS-00
CC
     Ted (Entrymee)
     Seption pross-reference(s): 7, 11, 17
ST
     deitalž desaturase gone FAD2M Corytus; hadel deltalž desaturase gene
     FAREN
IΤ
     Genes (plant)
     EL: PSU (Biological study, unclassified); PRE (Properties); BICL
     (Biclogooal study)
        .PAD: -U; cleare desaturase product of PADE-N gene of hazel and
        ita waka)
ΙT
     INA sequences
     cDNA secrimices
        ifir .DELTA.12 desaturase of hazel; oleate
        desaturase product of PAD. -Notene of hazel and its uses
     Fats and Alyceridic oils, biological studies
     EL: AGA. (Agricultural use); BOC (Ficlogical codurrence); FFD (Foed
     or feed user; BIOL (Biological study); OCCU (Occurrence); USES
     тОзеві
        That last, elemina of desaturase gene for altering
      fatty acid profile of; cleare
      desaturase product of PAD2-M gene of hazel and its uses)
ΙΤ
     Fatty smids, kip.opidal studies
     RL: ASE (Agricultural wase); BOC (Biological occurrence); FFO (Food
     or feed use; BIOL (Biblogical study); OCCU (Occurrence); USES
        of hazel, of ming of desiturase gene for altering profile of;
        cleare desaturase product of PAD2-N gene of hazel and its uses)
IT
     Protein sequence:
         cf .DELTA.12 desaturase of hazel; bleate
         desafurase product of FADM-M gene of hazel and its uses;
ΤТ
     Hazel (Corylus avellana)
         cleate desaturase product of FAD2-N gene of hazel and its uses)
ΙT
     Endoplasmic reticulum
        (.DELTA.12 desaturase of nazelnut; oleate
                            KATHLEEN FULLER BT/LIBEARY 308-4290
```

```
desaturase product of FADS-N mone of hizel and its uses)
ΙT
      196217-78-4
      EL: AGR (Agricultural use); ESU (Biological Study, unclassified);
      PRP (Properties); BIOL (Buol glos) study); USES (Uses)
          (amino abid sequence; deste desaturase product of FAD. -N gene of
          hadel and its uses)
ΙT
      196217-80-8
      EL: BOY (Biological study, unclassified); PEP (Properties ; BIOL
      (Biological study)
          (amino acid sequence; eleate desaturase product of FALC-N gene of
         nacel and its uses)
      1 9621 : = 77 = 3
                      19-217-79-5
                                       196317-11-3
ΙT
      EL: ASS (Agricultural use ; BSU (Biological study, unplessified);
      ETU (Biological use, unclissified); PAP (Proporties); BIOL (Biological study); USES (Uses)
          (nucleatize sequence; pleate dessturable product of FAD -N gene of
          nadel and its uses)
      59929-36-1, Oleane desaturase
      FD: BSU (Biological study, unclassified); PEP (Properties); BIOL
      (Biological study)
          (bleate desaturase product of PADS-N gene of hazel and its uses)
                                                                                   M. Carrel
L24 ANSWER 3 OF 19 HOAPLUS COPYRIGHT 1997 ACS 1997:518059 Topument Mo. 127:187034 Plants having mutant
      sequences that confer altered fatty acid
      H.-T. Willier. FCT Int. Appl. WO 9721-40 Al <u>970619,</u> 37 pp.
IESIGNATED STATES: W: Al, AM, AT, AV, AN, BB, BG, BR, BY, CA, CH,
     CH, CU, DE, DH, RE, ES, FI, GB, RE, HU, DI, IC, CP, RE, MG, RP, RR, RU, EM, LE, LS, ST, LU, LU, MD, MG, MM, MM, MW, MK, MG, MG, PL, PT, EG, ET, SD, SE, DG, SI, SM, TJ, TM, TB, TT, UA, UG, UG, UG, VN, AM, AU, EY, MG, MG, MG, MU, TM, EM; AT, BE, BF, BJ, CF, CG, CH, CI,
     CM, DE, DK, BD, FI, BR, GA, GB, DR, TE, DT, DU, MC, ML, MR, ME, NL, ET, SE, SN, TD, TG. (English). CODEM: PIXXD:. APPLICATION: WO 8-45.1189 361214. PRICEDTY: US 95-17.000 351214.
     Sweds, plants and oils are provised having low FDA sats., high oleic
AB
      a md, low limmle.c adid,; high or low paintify acid, low otearid
     actio, and low linoleid and plus linclened add, and advantageous
      functional or mutritional properties. Functs are disclosed that
      centain a mutation in a delta-12 or
      delta-15 fatty acid
      desaturase gene. Preferred plants are rapeseed and
sunfl wer plants. Plants garrying such mutant genes have
      after a fatty acid componing seeds. In one
     erbodiment, a plant contains a mutation in a region having the conserved motif His-Kaa-Kaa-Kaa-His, found in delta-
      12 and delta-15 fatty
      acid desaturases. A preferred mitif has the
      sequence His-Glu-Cys-Gly-His. A preferred mutation in
      thus motif has the amino acid sequence Hase-Lyn-Cys-Gly-His. Nucleic
      acid transents are discloved that comprise a mutant
      delta-12 or delta-15
      fatty acid desaturase denn sequence.
      ICM ADDEDDESS
IC
           A01H005-10; A01H001-40; C12N015-00; C07C057-02; C07C057-03;
      I (13)
           0070353-126
      1 -9 Find and Food Chemistry)
CC
      Secti n cross-re:erence(s): 11
      fatty acid profile alteration plant
      mutation; brassina fatty acid profile
      alteration mutation; Helianthus fatty
      acid profile alteration mutation
IT
      Pollination
```

```
(cross; plants having mutant sequences that confer
        altered fatty acid profiles)
ΙΤ
     Genes
     PL: BAC (Bitlogical activity or effector, except adverse); BIOL
     (Biological study)
        (microsomae; plants having mutant sequences that confer
        altered fatty acid profiles;
     Brassida dampestria
ΤT
     Frassida napud
     Cruciferae (Brassicaceae)
     Helianthus
     Mitadenesis
     Mutation
         (plants having mutant sequences that confer altered
      fatty acid profiles)
ΤT
     Fatty acids, hiplogical studies
     FD: FOC (Bitlegital occurrence); BPR (Biological process); BIOL
     (biological study); 0000 (Obournence); PROC (Process)
        (plants having mutant sequences that sinfer altered
      fatty acid profiles)
     Ungetable oils
IT
     Fig. 850 (Biological communetts); EEM (Remival or disposal); BIOL
     Chiclogical study); 0000 (Openmende); PROC (Process)
         (plants having mutant sequences that confer altered
      fatty acid profiles)
TΫ́
     Canala oil
     FL: BBR (Biblegical process); BIOL (Biblourdal study); BROC
      (Process)
        (plants having mutant sequences that denfer altered
      fatty acid profiles)
                                        71427-04-8, .DELTA.
     vu=80=9, Ethylmethanesulfonate
TΤ
     15-Fatty acid desaturase
     01536-70-0, .DELTA.12-Fatty
     acid desaturase 132831-61-7
                                        190591-62-6
     190691-63-7 190891-64-8
     FM: PAC (Biological activity or effector, except adverse); BIOL
     (Bucunginal study)
        (plants having mutant sequences that denfer altered
      fatty acid profiles)
     142889-74-0 192889-75-1 18.8889-76-4 192889-79-5
TT
                               19. #83-76-2 192889-77-3
                                190883-30-3 192889-81-9
     FD: BAC (Biological activity or effector, except adverse); BPR
     (Biclogical piccess); BIOL (Biological study); EROC (Process)
        (plants having mutant sequences that dinfer eltered
      fatty acid profiles)
ΙT
     fT-10-3, Falmitic acid, biclosical studies - 57-11-4, Stearic acid,
     biological studies (60-33-3, Lincleid ad.d, biological studies
     112-80-1, Oleic acid, biological studies =468-40-1,
     .alpha.-Binclenic adid
                                1929/3-84-4 19 323-55-5
     198633-507-7 198623-58-6
     Fb: BOC (Biological pocurrent); F101 (Bi dogidal study); OCCU
     Madmar ner. ce i
        (plants having mutant sequences that domfer altebed
      fatty acid profiles)
L24 ALLWER 4 OF 1 HOAPLUS COPYRIGHT 1997 ALS
1997: Plass - Combument No. 126:289:96 | Microbial and plant genes for
     .DEDTA.6-desaturases and their use in increasing tibsue levels of
     .pamma.-limelenic acid. Thomas, Terry L.; Recdy, Arutu S.; Nuccio,
     Michael; Numberg, Andrew N., Freyswinet, Jeorges L. (Shone-Poulond
     Approximis, Fr.). U.S. US 5614591 A 970325, 30 pp. Cont.-in-part of U.S. 5,588,506. (English). CODEN: USKKAM. APPLICATION: US 94-366779 941250. PRIORITY: US 91-074475 311(10; US 92-817919 320168; US 93-953952 921015; US 94-367382 940914.
                             KATHLEEN FULLER BT/LIBRARY 303-4290
```

```
AB
    Microbial genes for .DELTA.6-desaturases are cloned and
     characterized for use in the prepn. of transgenic organisms
     synthesining high levels of .pamma.-linelenic acid from lineleic
     abid. Plants expressing a desaturase gene and with high tissue
     levels of .gamma.-linclenic acid are chilling resistant. These
    plants can also be used to produce bils with altered levels
     .gamma.-finalence acid. The Symechicystis .DELTA.6-desaturase was
     clone: by expression in a .gamma.-linelenate-deficient Anabena.
     Expression of the gene in transgenic tobacco and carrot is
     demonstrated.
    ICK: 12::015-83
IC
          112N018-82; C12N001-21; C12P007-64
NCL
    435134000
     7-1. (Enzymes)
CC
ST
     delta: desaturase gene Synechicoyatia borage; gamma linolenate manuf
     delta: desaturase
     Plasmad vectors
TT
        (1.1.1.1.DELTA.6NOS, borage .DELTA.6-desaturase gene on, expression
        in pairet dell culture and tobacco of; microbial and plant genes
        for .DELTA.6-desaturases and their use in increasing tissue
        levels of .gamma.-linosenic acid:
     Plasmid vectors
TΤ
        (2.1..DELTA.6NOS, borage .DELTA.6-desaturase gene on, expression
        in carret dell culture and tobacco of; microbial and plant genes
        fir .DELTA.6-desaturases and their use in increasing tissue
        levels of .gamma.-lino.enic acido
TT
    Carrot
        (rell cultures as expression host; microbial and plant genes for
        .DELTA.6-desaturases and their use in increasing tissue levels of
       Joan
TT
     Bilamentous fungi
     Pearcat
     Eagle [plant]
    Soybean
    Sunflower
     Lobacino
        Temprossion host; microbial and plant genes for
        .DELTA.6-desaturases and their use in increasing tissue levels of
        .damma.-linclenic acid
    Anabacha
TΤ
       Tempoyasion of .DELTA.6-desaturase genes from carboxylase
       primoter of; microbial and plant genes for .DELTA.6-desaturases
       and their use in increasing tissue levels of .gamma.-linolenic
       actd)
    Glycinins
ΙT
     RL: MSC (Miscellaneous)
        tempression of .DELTA.6-desaturase genes from promoter of gene
        for; microbial and plant genes for .DELTA.6-desaturases and their
       use in increasing tissue levels of .gamma.-linolenic acid)
T T
     350 promoter (penetic element)
     EL: B"U "Biblogical use, unclassified); BIOL (Biological study);
     SEC 33-31
        empression of .DELTA.6-desaturase genes from; microbial and
        plant genes for .DELTA.6-desaturases and their use in increasing
        tiusu- levels of .gamma.-linolenic acid)
     DNA siguinales
        for .DELTA.6-desaturase of Synechocystis; microbial and plant
       qches for .DELTA.6-desaturases and their use in increasing tissue
        levels of .mamma.-linolenic acid)
ΙT
     cDNA sequences
        for .DELTA.6-desaturase of borage; microbial and plant genes for
        .DELTA.6-desaturases and their use in increasing tissue levels of
        .gamma.-linolenic acid)
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ΙΤ
     Genes (microbial)
     Genes (plant)
     PL: BUU (Biological use, unclassified); PRP (Properties); BIOL
     Bi:logical study); USES (Uses)
        ofor .DEDTA.6-desaturase, cloning and expression of; microbial
        and plant denes for .DELTA.6-desaturases and their use in
        increasing tissue levels of .gamma.-linolenic acide
     Globulins, miscellaneous
ΙT
     BL: MSC | Hisbellanebus)
        chelianthinins, expression of .DELTA.6-desaturase genes from
        promoter of dene for; microbial and plant denes for
        .OELTA.6-desaturases and their use in increasing tissue levels of
        .gamma.-linolenio acid)
    Globulins, miscellaneous
ΙT
     BL: MSC (Miscellaneous)
        (meliar.thins, expression of .DELTA.6-dusaturase genes from
        promoter of gene for; miorobial and plant genes for
        .(EDTA.0-desaturases and their use in increasing tissue levels of
        . gamma.-linolenic acido
     Erometer (denetid element)
TT
     SL: FUU (Biological use, unclassified); BUOL (Biological study);
     USES (Uses)
        (nemologous and neterologous, expression of .DELTA.6-desaturase
        genes from; migrobial and plant genes for .DELTA.6-desaturases
        and their use in increasing tissue levels of .gamma.-linglenic
        5 (i i)
ΙŢ
     Albumins, misdellanecus
     FL: MSC (Misbellaneous)
        chapins, expression of .OELMA.8-desaturase genes from promoter of
        gone for; midrobial and plant genes for .DELTA.6-desaturases and
        their use in increasing tissue levels of .gamma.-Linclenic acid)
     Erst in sequences
ΙΤ
        ( f .DELTA.6-desaturases of Symeonocystis and borage; microbial
        and plant genes for .DELTA.6-desaturases and their use in
        increasing tissue levels of .gamma.-linolenic abid:
ΙT
    Cold stress (plant)
        (transpenie plants resistant to; mioredual and plant genes for
        .!ELTA.6-desaturases and their use in increasing tissue levels of
        . mamma.-linolenio adid
     Borage officinalis
IT
     Syne thodystis
        (.CELTA.6-desaturase gene of; microbial and plant genes for
        .TEDTA.6-desaturases and their use in increasing tissue levels of
        . pamma.-linclenic acid:
ΙΤ
     148734-39-8 180583-92-0, Desaturase, linoleate
     (Borago dificinalis)
     Fh: AGR -Agricultural use:; BSU (Biological study, unclassified);
     FRP (Eroperties); BIOL (Biological study); USES (Uses)
        (amino acid sequence; microbial and plant genes for
        .1BLTA.6-desaturases and their use in uncreasing tissue levels of
        .:amma.-linolenic acid)
     9031-33-4, Carboxylase
IΤ
     FL: MSC (Miscellaneous)
        (expression of .DELTA.6-desaturase genes from Anabena promoter of
        gene for; microbial and plant genes for .DELTA.6-desaturases and
        their use in increasing tissue levels of .gamma.-linolenic acid)
     7142 -04--9, .DELTA.15-Desaturase
TT
     8462 - 21-4P
     FL: ASR (Adricultural use); BPN (Biosynthetic proparation); FRP
     (Properties); BIOL (Biological study); PREP (Preparation); USES
     (Uses)
        (gene for, in engineering fatty acid
        profiles; microbial and plant genes for .DELTA.6-desaturases and
        their use in increasing tissue levels of .gamma.-linolenic acid)
                           KATHLEEN FULLER BT/LIBRARY 308-4290
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ΙΤ
     91275-16-9P, Octadecatetraenoic acid
     F.L.: BFM (Biosynthetic preparation); FTGL .Biological study); FREP
      (Preparation)
         (manuf. with transgenic microorganisms, .DELTA.6-dusaturase genes
         in; microbial and plant genes for .DELTA.\ell-desaturases and their
      use in increasing tissue levels of .qarma.-linolenio acid) #082-66-0P, .DELTA.6-Desaturaso
ΙT
     FL: AGE (Agricultural use); BEW (Bicsynthetic preparation); PEP
      Properties); BIOL (Billogical study); PREP (Preparathon); USES
      Theres:
         unicrobial and plant genes for .DRIMA. \theta\text{--}desaturases and their use in increasing tissue levels of .pamma.-linolenic asid:
ΙT
     463-46-1, .alpha.-Lindlenic acua
     AG: BGY (Biological study, unclassified); BIOS (Biological study)
         undersorganisms producing, manuf. of .gamma.-linolemate with;
        microbial and plant genes for .DELTA. (-decaturases and their use
         in increasing tissue levels of .gamma.-linclenic acid)
     1:0093-90-3 1:0533-91-9 19:093-60-0
ΙT
     BB: AGE (Agricultural use); BSU (Bibliogroul study, unclassified);
     FRP (Freperties.; BIOL (Biological study.; USES (Uses.
         (nucleatide sequence; midrobial and plant genes for
         .DELTA. 6-desaturases and their use in increasing tissue levels of
         .gamma.-linolenio acid)
     506-26-38, .gamma.-Linelenso abid
ΤT
     RM: AGR (Agricultural use); SPU (Billymthetic preparation); SPOD
      Buoligical study); PREP (Preparation); UVES (Uves)
         sprepr. from lineleid anid of; mincheal and plant genes for
         .DEDTA.6-desuturases and their up in undreading traspe levels of
         .domma.-linotenio abido
     +0- (\frac{1}{2}-\frac{1}{2},-\frac{1}{2},-\frac{1}{2}-\frac{1}{2}) tradecadiencie (cid (0,Z -, reactions
ΙT
     FL: FCT (Readtant)
         a.cammaa.-linolenio acid prepo. from; rucrobial and plant denes
         for .DEDTA.6-desaturases and their use in increasing tissue
         levels of .gamma.-linclenic acid:
L24 ANNWER 5 OF 19 HOAFINS COPYRIGHT 1:37 ACS
1997: LB. 81 - Bostament Nt. 128: 99447 | Temperature - regulated mRNA
     accomplation and stabilization for fatty acid
     desaturase genes in the syanchasterium Symethodocous sp.
     strain POC TIME. Sakamote, Techio; Pryant, Dinald A. (Department of
     Blochemistry and Molecular Biology, The Fennsylvania State
     Phomersity, University Park, PA, 168-2, UNA). Mod. Moortbiol.,
     . 5(+), 12-1-12-20 (Enalish) 1994. COMEN: MOMIEE. ISSN: 1950-982X.
     Indulianer: Blackwell.
AΒ
     Cyanobacteria addimate to low-temp. condutions by desaturating
     their membrane lipids. The de.B. .thega. desaturase, and desC
      1.DENTA.9 desaturase) gener of Symechococcus sp. strain ECC 7002
     were cloned and characterized, and the empression of the desA (.
     DELTA.12 desaturase), desB and desC gener was
     obtudied as a function of temp. The steady-state mEMA abundance for
     the desA gene was threefplu nigher in bells grown at 32.degree.C
     than in calls grown at St. decree.C. Desk transcripts were not detected at Fr.degree.C. but were abundant in calls grown at .2. degree.C. Levels of desC mENA were sumilar at both growth temps.
     The mEMA levels of each desaturase gene increased within 15 min of a
     temp. snift-gown to 22.degree. 1, and reMA level, recovered within 15
     min after a shift-up to 38.degree.C. The cold-induced accumulation
     of transcripts from the dezA and desb genus was suppressed by the
     addr. of chloramphenical, but the transport elevation of the desC
     transcript levels at 22.degree.C was not affected by
     chloramphenical. The half-lives of the desA and desB mENAs were significantly larger in sells grown at 2. degree. I than in cells grown at 38.degree. C, but the desC mENA had a similar half-life at
     both temps. These studies reveal three patterns of temp. regulation
```

CC

ST

ΙT

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ΙT

TT

```
for the desaturase genes, whose expression is tightly controlled by
     a combination of mRMA synthesis and stabilization. These studies
     demonstrate that elevation of desaturase mRNA levels is not the
     nate-limiting event during the low-temp. addlimation of
     cyanobasteria.
     10-1 (Microbial, Algal, and Fungal Biochemistry)
     Section on ssereference(s): +
     Stme moded has fatty acid desaturase
     general se poembe
     Genesa (miprobial)
     RI: PEP - Properties
         desA; temp.-regulated mEMA accumulation and stabilization for
      fatty acid desaturase genes in
        yan-drafterium Synechococous sp. strain PDC 7002)
     Genes (mibrobial,
     Fil: PF.P (Properties)
         wesh; temp.-regulated mEMA abdumulation and stabilization for
      fatty acid desaturase genes in
        syanobasterium Synechodoccus sp. strain POC 7000)
     Genes (midrabla)
     PD: FRP /Properties
         desC; temp.-regulated mEMA accumulation and stabilization for
      fatty acid desaturase denes in
        syanoba sterium Synechodocous sp. strain PCC 7001)
     SMA sequences
     Exprein semiendes
     Byrandha roamas
     Temperature effects (biological)
         temp.-regulated mRIM appumulation and stabilization for
      fatty acid desaturase genes in
        oryanchasterium Synechopopous sp. strain PCC 7001.
     n.F.NA
     FD: IPP (Picperties)
        themp.-regulated mANA accumulation and stabilization for
      fatty acid desaturase genes in
        cyanchacterium Symechockocus sp. strain PCC 7301,
     156532-36-4
     BD: PFF (Properties)
        Caming acid secuence; temp.-regulated mENA accumulation and
        mabilination for fatty acid
      desaturase genes in cyanobacterium Synechoococus ap.
        ntrain, FCC 7002)
     105402-16-1, GenBank D03773 183176-13-2, GenBank U36389
     109178-00-1, GenBank UN6891
     F1: FFE (Properties)
         nucreatide sequence; temp.-regulated mENA accumulation and
        stabilization for fatty acid
      desaturase genes in cyanobauterium Synechoococus .p.
        mrain ECC 7002)
     34 14-34-6, Fatty acid desaturase
     EL: IFP (Properties,
        -temp.-regulated mENA argumulation and stabilization for
      fatty acid desaturase denes in
        cyanobacterium Synechoologus sp. strain POC 710.
L24 ANSWER 6 OF 19 HOAPLUS COPYRIGHT 1997 ACS
1996;7^\circ Do. 2^\circ Document N _2 . 126:115911 The F-OLE1 gens of Pichia angusta
     endedes a .DELTA.9-fatty acid desaturase
     and complements the old mutation of Sappharemydes
     corevisiae. Anamnart, Sarintip; Tomita, Tetsushi; Fukui, Fumio;
     Fujimori, Ho; Harashima, Satoshi; Yamada, Yasuniro; Oshima, Yasuji
     (Department of Biotechnology, Faculty of Engineering, Osaka
     University, 2-1 Yamadaeka, Suita-shi, Osaka, 265, Japan). Gene,
     104(2), 290-336 (Engli h) 1997. CODEN: GENED6. ISSN: 0578-1119.
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MATHLEEN FULLER BT/LIBRARY 308-4290

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Publisher: Elsevier.
AB
     Three PCR-amplified DNA fragments hyporidizing with the OLE1 gene
     encoding .DELTA.9-fatty acid desaturase
     of Saccharomyces cerevisiae were obtained using, resp., genomic DNAs
     of one strain each of Kluyveromyces thermotolerans, Pichia angusta
     and Yarrowia lipolytica as templates. A gene designated P-OLE1 was
     clined from the above fragment of P. angusta and sequenced. An open
     reading frame of P-OLE1 encodes a 44.6-kDa protein consisting of 451
     amino abid residues, which shows high identity (62) and similarity
     (i9) to that deduced from the OLEI hadleotide sequence. Expression
     of P-OLE1 driven by the S. derevising GAP promoter or its own
     primitter complemented the olel mutation of S. derevisiae.
     Transcription of 9-0LE1 in the native host was suggested to be
     partially repressed by cleid acid in the medium, as was that of OLE1
     in S. derevisiae and a similar yene in Y. lipolytica, but that of a
     similar gene in W. thermatolerans was not.
CC
     3-3 (Bibmhemidal Genetics)
     Section pross-reference(s): 7, 10
ST
     POLE1 gene fatty acid desaturase
     sequence; Fichia fatty acid desaturase
     dene sequence
ΙΤ
     Genes (midrobial)
     EL: ANT (Analyte): BPR (Biological process): BPP (Properties): ANST
     (Amalytical study); BIOL (Biological study); PROC (Process)
        (E-DLE1; the E-ODE1 gene of Pichia angusta encodes a .DEDTA.9-
      fatty acid desaturase and complements
        the olel mutation of Saddharomydes derevisiae)
TT
     Erotein sequences
        (ci Pichia angusta .DEDTA.9-fatty acid
      desaturase 7)
TT
     DMA seguences
        (of the E-OLE1 gene of Pichia angusta encoding a .DELTA.3-
      fatty acid desaturase and
        complementing the blel mutation of Backhardmydes
        derevisiae)
ΙT
     Bichia angusta
     Saccharomyces cerevisise
        (the P-CLE1 gene of Pichia angusta encodes a .DEDTA.3-
      fatty acid desaturase and complements
        the olel mutation of Saodhardmydes derevisiae)
     112-36-1, Cleic acid, biological studies
ΙT
     FL: BAC (Biological activity or effector, except adverse); BIOL
     (Fiological study)
        (F-OLE) gene of Fighia angusta encoding a .DEDTA.9-fatty
      acid desaturase and complementing the olel
      mutation of Jacoharomyces derevisiae repressed by oleic
        acidt
IT.
     186208-06-0:
     FIG. EAC +Biclogical activity or effector, except adverse); PRP
     (Properties); BIOL (Biological study)
        (amino acid sequence; the P-OLE1 gene of Pichia angusta encodes a
        .DEDTA. P-fatty acid desaturase and
        complements the flel mutation of Saccharomyces
        derevisiae)
ΙΤ
     186209-56-3
     EL: FEE (Properties)
        (nublectide sequence; the P-OLEI gene of Pichia angusta encodes a
        .DELFA. 3-fatty acid desaturase and
        complements the olel mutation of Saccharomyces
        cerevisiae)
ΙT
     \mathbb{P}(14-34-3), .DELTA.9-Fatty acid
     desaturase
     RL: BAC (Biological activity or effector, except adverse); PRP
     (Properties); BIOL (Biological study)
                           RATHLEEN FULLER BT/LIBRARY 308-4290
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(the P-OLE1 gene of Pichia angusta empodes a .DELTA.9-
      fatty acid desaturase and complements
         the olel mutation of Saccharchydes derevisiae)
L24 ANSWER 7 OF 19 HOAPLUS COPYRIGHT 1997 AGS
     23.644 Decument No. 124:379.93 Isolation and characterization of an Arabidopsis traliana obNA encoding a .DEDTA.7-stero1-0-5-decaturase by functional complementation of a defective yeast
     mutant. Gasnotte, Daniel; Husselstein, Tania; Bard, Martin;
Lasroute, Francois; Benveniste, Puerre (Department de Biologie
Cellulaire et Moleculaire, Institut de Botanique, Strasbourg, 67033,
     Fr.). Plant J., 9(3), 391-9 (English: 1996. CODEN: PLIUED. ISSN:
     09400 - 7412.
     A yeast hull mutant (erg 3) defective in BBO 3, the gene
AB
     emboding the C-5 sterol desaturase required for ercosterol synthesis
     was transformed with an Arabidopsis thaliana cDNA library inserted
     in a yeast vector. Transformants (4.1 ines.10%) were screened for
     cycloheximide (CR) resistance and 400 possible clones were analyzed
     to det. their sterol profile. How levels of ergosterol in addn. to
     .DEDTA.7- and .DELTA.8-stercls normally present in erg3 were
     is Cated in three yeast transformants. Characterization of one
     transformant indicated a cONA of 1141 bp. Transformation of an erg fixtrain with this plasmid led to CH resistance, hystatin sensitivity and an ergosterol profile. After sub-cloning in a
     pBluescript vector and subsequent segmending, an CRF of 843 bp
     er moding a possible 291 amino acid polypeptide was deduced. Three
     histodine-rich motifs (BKIB, BK2BH and BK2BH; were found in the A.
     thaliana CEF which are also present in the yeast EEG 3 gene. These
     histidine-rich motifs are also characteristic of many membrane-bound
     fatty acid desaturases from higher
     plants. These data strongly suggest that the A. thaliana cDNA
     encodes a .DELTA.7-steroi-C-3-desaturase.
     3-3 (Piochemical Genetics)
     Section ordes-reference(s): 7, 11
ST
     Anabidopsis sterol desaturase bDMA sequence gene
ΙT
     Gene, plant
     RL: FRF (Eropenties)
         (for C-f stero) desaturase; is lation and characterization of
         Arabidopsis thaliana cDNA -nooding .DELMA.7-sterol-C-1-desaturase
         by functional complementation \rightarrow t defective yeast mutant
     Arabicopsis thaliana
ΙΤ
     Protein sequences
         (isolation and characterization of Arabidopsis thaliana cDNA
         encoding .SELMA.7-stepol-C-5-desaturase by functional
         complementation of defective yeast mutant.
     Deckyribonucleic acid sequences
ΙT
         occmplementary, isolation and sharacterization of Arabidopsis
         thaliana dDNA encoding .DELMA. -store.-C-i-desaturase by
         functional complementation of defective yeast mutant)
     175960-67-5
IT
     EL: PEP (Properties)
          amino acid sequence contq. three histidine-rich motifs;
         isclation and characterization of Arabidopsis thaliana cONA
         encoding .DELTA.7-steril-C-f-mesaturase by functional
         complementation of defeative yeast mutant
     372°5-37-1
EL: BUU (Biological use, unclassified); BIOL (Biological study);
          isolation and characterization of Arabicopsis thaliana SDNA
         encoding .DELPA.7-sterol-C-5-desaturase by functional
         complementation of defective yeast mutant)
ΙT
     170611-11-7, Genbank X90454
```

FL: PFP (Properties)

```
(nucleotide sequence; isolation and characterization of
        Arabidopsis thaliana cENA encodin: .DELTA.7-sterol-C-5-desaturase
        by functional complementation of objective yeast mutant
L24 ANSWER 3 OF 19 HCAPLUS COPYRIGHT 1 07 ACS
1995:235509 Document No. 127:750097 Molycular cloning of cDNA for
     fatty acid desaturase of Anacystis
     midulans and its use in preating transgenic plant resistant to cold
     temperature. Nish:zawa, Osamu; Toguet, Toshihiro (Hirin Beer K. K.,
     Capan). PCT Int. Appl. W0 9518212 Al 950706, 41 pp. DESIGNATED
     STATES: W: AM, AU, BB, BG, BF, BY, CA, CU, CZ, FI, GE, HU, JE, KG, FR, KZ, LK, LT, LV, MD, MG, MH, MO, UL, PL, RO, RU, SI, SK, TI, TT, UA, US, UN, VH; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES,
     FE, GA, SB, GR, IE, IT, LU, MC, ML, ME, NE, NE, FT, SE, SN, TO, TG.
     (Japanese). ODDEM: PINKER. APPLICATION: WO 94-JP2288 941228.
     PRIÓRITY: JP +3-353656 931229.
ΑВ
     Gene des 9 var fragment of Anabacha variabilis IAM N-5 is isolated
     upstream in m gene desA that encodes .DELTA.-12
     -unsaturage and used as a probe for the isolation of open reading
     frame (ORF) des à nid if Anadystis nivulans. ORF des à nid bodes
     for a desaturate desaturating the .DRLMA. -position of a fatty acid
     bound to a lipid and exhibits 50 and 30% similarity to gene des 9
     var of Anabaena variabilis and steam yi-C-A unsaturase of mouse,
     resp. The CEF introduced into transferio tobacco plants increased
     the montent of unsato, fatty words and the resistance to cold temp.
     ICM | C13N | 11 -75
IC
     103 | Clando: -00; A01H001-00; A01H008-00
ICA CLENOSP-S
CC
     T-3 (Enlaymen)
     Section props-reference(s): 11
ST
     Anacystis fatty acid desaturase SDNA
     sequence; cela resistance des Binid Anacystus; transgenic plant
     unsatd fatty Adid
ΙΤ
     Gene, plant
     FL: AGE (Agricultural use); FEE Properties; BIOL Biological
     study); TDEN (Uses.
         Dues 3 nod; cloning of cDNA for .IELTA.9-fatty
      acid desaturase of Anadystis nistilans and its
        use in dreating transpenic plant resistant to sold temp.)
IΤ
     Trotein sequences
         \mathbb{P}(f) . DELTA, \mathbb{H}-fatty acid desaturase
        or Analy-tis niquians
     Flant reli
IT
     Elant
     Tcbsabble
         transmenio; empression of cDMA for .DFLTA.9-fatty
      acid desaturase of Anadystis nichulans inc
ΙT
     Temperature effects, biological

    sold, empression of SMA for .DELTA.9-fatty

      acid desaturase of Anacysti, nichland in
        transgemic plants to increase resortance to)
ΙT
     Deoxyribonulleid adid sequences
         cromplementary, for .DELTW.9-fatty acid
      desaturase of Analystis miduland)
ΙΤ
     Pattly adids, miscellaneous
     RL: MSC (Miscellarwous)
        Consat (., expression of cDNA for .DELTA.3-fatty
      acid desaturase of Anacystic nitulans in
        transquard plants to increase content (f)
     168613-13-6
     EL: AGE (Agricultural use); PEP (Properties); BIOL (Biological
     study); UNES (Uses)
        (amino acid sequence; cloning of DNA for .DELTA.9-fatty
                             MATHLEEN FULLER BT/LIBEARY 308-4290
```

```
acid desaturase of Anacystis nidulans and its
        use in creating transdenic plant resistant to cold temp.)
     166322-04-3
TT
     PL: AGE (Agricultural use); PRE (Properties); PIOL (Biological
     study); USES (Uses)
        (nucleotide sequence; cloning of cDNA for .DELTA.9-fatty
      acid desaturase of Anacystis midulans and its
        ame an preating transferric plant resistant to cold temp.)
L24 ANSWER + OF 19 HOAPLUS COPYFIGHT 1997 ACS
1995:273449 | Deciment No. 127:29803 | Identification of a gene that
     complements an Arabidopsis mutant deficient in chloroplast
     .cmeda.0 desaturase activity. Falloome, Deane L.; Gibcon, Susan;
     Demieux, Bartrand; Somerville, Chris (Dep. Plant Biol., Carnegie
     Inst., Chanford, CA, 94% 5, USA). <u>Plant Physica., 106(4), 1453-9</u> (<u>English) 13:4. COOEN: PLEHAY. ISSN: 0682-0889.</u>
    Membrane lipteds of the fade (formerly fade) mutant of
AB
    Arabado, sis, which is deficient in chloroplast .cmega.6 desaturase
     activity, have increased levels of monounsatd. fatty
     acids and are deficient in trienoid fatty
     acids. A gutative face cDNA clone was isolated by probing a
     COMA library with a degenerate oligonuclectide based on a conserved
     region within known .cmega.3 desaturase genes. Expression of the
     oSNA in transgeric plants of a fact mutant restored normal
     levels of all fatty acids. When used as a
     hybridication probe, the cDMA identified a restriction
     fragment-length polymorphism that co-segregated with the fade
     mutation. Thus, on the basis of a genetic complementation
     test and genetic map position, the fad6 dene is encoded by the cDNA.
     The GINA encoded a 41%-amin; spid polypertide of 47,7.7 D that
     displayed a high degree of sequence similarity to a .DELTA
     .12 desaturase from the Hyanobapterium Synechopystis. The
     facé dend exhibited less sequence nomol, to any known higher plant
     desaturuse, including an endoplasmic reticulum-locatioed .omega.6
     desaturase corresponding to the Anabidopsis fad2 gene.
     7-5 :Encymes.
CC
     Sectuan orese-reference(c): 3, 11
ST
     fatty acid in equal desaturase sequence
     Arabiacopwis; cDNA omegaé desaturase sequence Arabiacopwis
     chloroplast; gene fadé sequence omaga6 desaturase Arabidopsis
TT
     Gene, blant
     EL: PEP (Properties)
        (tage; identification of gene that complements Arabidopsis
      mutant definient in onlogolast .omeda.o desaturase
        sertimaty)
TT
     Arab.dopsis inaliana
     Chimplast
     Irea f
     Protein bequences
        (.nentification of gene that complements Arabidopsus
      mutant deficient in enformplast .omega.6 desaturase
        antivity)
     Fatty acids, biological studies
TT
     Rh: BDC (Biological occurrence); MFM Metapolic formation); BIOL
     -Bab.od.bal study); FORM (Formation, nonpreparative); OCCU
      Jackro-noet
        ridentification of gene that complements Arabidopsis
      mutant definient in emberoplast .omega.6 desaturase
        a:timity)
ΙT
     Deoxyriponusteic acid sequences
        complementary, identification of gene that complements
        Arabidopsis mutant deficient in chloroplast .omega.6
        desaturase activity)
     163961-98-6
```

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PL: BAC (Piological activity or effector, except adverse); PRP
      Properties); BIOL (Fiblogical study)
         identification of gene that complements Arabidopsis
      mutant deficient in chloroplast .emega.6 desaturase
         activity)
     66819-61-4, Fatty acid .cme;a.6-
ΙT
     Desaturase
     FL: BOC (Biological occurrence); MFM (Metabolic formation); BIOL
      -Biological study); FORM (Farmation, nonpreparative); OCCU
      (Octobal remova)
         : Identification of gene that complements Arabidopsis
      mutant deficient in the riplast lomedalő desaturase
ΙT
      118670-84-6, GenBank U19 08
     F.L.: PF.P (Froperties)
          nurlectide sequence of; identification of mene that complements
         Arabidopsis mutant delicient in chloroplast .omaga.6
        Hesaturase activity)
L24 MISWER 10 OF 19 HOAPLUS COPYRIGHT 1997 ACS
              Ducument No. 127:124842 Cloning of .mega.2 desaturase
1995:1 6174
     from cyanobacteria and its use in altering the degree of
     reminanc-lipid insaturation. Sakamoto, Toshio; Los, Dmitry A.;
     Higushi, Thoichi: Wada, Hattme: Nishida, Ikuo: Ohmori, Masayuki:
     Murate, Mirio (Department Malecular Biomesmanics, Graduate
     University Advanced Studies, Okazaki, 444, Japan). Flant Mol.
     B.:1., 26<sup>2</sup>1), 249-03 (English) 1934. CODEN: PMBISB. ISSN:
     (167-441...
    Cyanobacteria respond to a decrease in temp. by desaturating
AB
     fatty acids of membrane lipids to compensate for
     the decrease in membrane fluidity. Among various desath, reactions
      in Gyanobarteria, the decath. of the Lomega.3 position of
     fatty acids is the most censitive to the change in
     temp. In the present study, the authors isolated a gene, designated \cos B_{\rm s} for the immegali desturase from the symmetrium,
     Symethictists sp. FCC 6608. The desB gene encodes a protein a 359 animo-actual residues with mil. mass of 41. kDa. The desB gene is transcribed as a menodistrenic operon that produced a single
     transcript of 1.4 db. The level of the dosb transcript in della grown at .7.degree, was 13 times higher than that in della grown at
     34.degre-.. To manipulate the fatty-acid
     unsath. It membrane lipids, the desB gene in Symeonocystis sp. PCC
     6-3: was mutated by insertion of a kanamydin-resistance
     gene cartingse. The resultant mutant was unable to
     desaturate fatty acids at the .omega. 3
     p_{\theta} satisfies. The desA gene, which encodes the .DELTA.
     12 deaturase of Syndonicystis sp. FCC 6817, and the dos8 gene were introduced into Syndonococcus sp. FCC 7942. While the parent cyanobacterism can ally desaturate membrane lipids at the
     .DENTA.9 position of fatty acids, the resultant
     transfirmant was able to desaturate fatty
     acids of numberane lipids at the .DELTA. 9, .DELTA.
     12 and . maga. E-positions. These results confirm the
     thm tion of the deals generally demonstrate that it is possible to
     openetically manipulate the fatty-acid unsath. of
     rembrane ...pids in cyanoba steria.
CC
     5-3 (Bipotemical Genetics)
     Section pross-reference :): 7, 10
ST
     cloning sequence omegab desaturase gene Synech cystis; Synechocystis
     desiturable alteration membrane lipid unsain; dene desB sequence
     ome (a3 delaturase Symeomocystis; transcription omegas desaturase
     gene Synephonystis temp; desaturase delta?2 omegas Synephonystis
     transformation Symechococcus
ΙT
     Symechicoccus
```

```
Transformation, genetic
         Alteration of membrane lipid unsath. in Synechococcus sp. PCC
        7941 by transformation with .omega.3- and .DELTA.
      12 desatirase genes from Synechopystis sp. F00 6803
ΙT
     Lipids, biological studies
     RL: MFM (Metabolic formation); BIOL (Biblidical study); FOSM
     (Formation, nonpreparative)
        (alteration of membrane Lipid unsath, in Synechopuccus sp. FCC
        7-4. by transformation with .emega.3- and .DELTA.
      12 desaturase genes from Synechopystis sp. FCC 6813:
ΙT
     Fatty acids, brological studies
     RL: MFM (Metabolic formation); BIOL (Biblical study); FORM
     ·Formation, nonpreparative:
        (changes in fatty acid compn. of total ligids
        upon transformation of Symechoporous sp. ECO 7942 with .omeda.3-
        and .DELTA.12 desaturase genes from
        Symmonicystis sp. ECO 6893)
ΙΤ
     Syne thooystis
        (blining and sequence of .omega.) desaturase from Synephococcus
        and its use in altering the degree of membrane-limid unsath.)
ΙT
     Cell memberane
     Decayribanualera said sequences
     Emotoin sequences
        off-ming and sequence of .omega.P desaturase from Symechocystis
        and its use in altering the degree of membrane-lipid unsath.)
ΙT
     Cyanthosoteria
        (oloning and sequence of .omega.) desaturase from dyanobacteria
        and its use in altering the degree of membrane-lipid unsath.)
ΙT
     Gene, microbial
     FL: BPR (Biological process ; PRR (Properties ; BIOL (Biological
     study); PROC (Process)
        class; claning and sequence of .imega.? desaturase gene desb from
        Symechococcus and its use in altering the degree of
        membrane-lipid unsath.)
TT
     Temperature effects, biological
        (temp. resulation of limegal) desaturase dene desb transcript
        lowels in Symechocystase
ΙT
     Ribonucleic actas, messender
     BL: MBM (Metabolic formation); BIOL (Biological study ; FORM
     (Formation, nonpreparative)
        comp. regulation of .cmega.? desaturase dene desP transcript
        I vels in Symechodystus)
ΙT
     Cene, midiobia.
     FL: PFH (Miological process); BIGE (Biological study); PROC
     (Promess)
        (desA, .DELTA.12 desaturase; alteration of
        mond rane lipid unsath. in Synephologopus sp. ECC 1941 by
        transformation with .omeda.3- and .DELTA.12
        or saturase genes from Symethodystis sp. PCC 6808)
ΙT
     7283+-16-1, .DELTA.12 Denaturase
     FL: RAC (Piological activity or effector, except adverse); BIOL
     (Bible sidel study)
        culteration of membrane ripid creats, in Symethodocous sp. PCC
        144. by transformation with .imega.i- and .DELTA.
      12 Wesaturase genes from Symechocystis sp. ECC 6303.
IT
     [7-1 -s, Hexadecanoid acua, biological studies |
                                                      57-11-4, € 18:0,
     riological studies (3)-33-3, 3,12-00tsdepadienord actic (2,2)-,
     kielogical studies 112-50-1, 9-Octadecenoic acid 10-, studies 373-49-9, 9-Hexadecenoic acid, (Z)=-463-40-1
                          113-50-1, 9-Octadesencic acid 30-, biological
     11-0 stade sension and (Z) = -5070-13-1, 9,12-Hexadecadienoid acid,
     -2, 2 - 23934-77-2, Obtadebadienvic abid (3, 7) - 32859-34-0
     EL: BOC [Biological occurrence]; MFM (Metabolic formation); BIOL
     'Biological study); FORM (Formation, nonpreparative); OCCU
     (Occurrence)
```

```
(changes in fatty acid compn. of total lipids
        upon transformation of Jynechoppopus sp. PCC 7942 with .omega.3-
        an:: .DELTA.12 desaturase genes from:
        Symethodystis sp. PCC 6803)
     7142^{6}-14-4, .DELTA.15 Des sturase
ΙΤ
     161027-24-3
     RL: BAC (Biological activity in effector, except adverse); PRP
      Properties); BIOL (Bislemeal study)
        coloning and sequence of .omega.b desaturase from dyanobacteria
        and its use in altering the degree of membrane-lipid unsath.
     1.002.14-15-7
ΙΤ
     FL: FPS (Fiblogical process); PRP (Properties); BICL (Biblogical
     roudy ; PROG (Erocess)
        ordening and sequence of .amega.b desaturase from dyanobacteria
        and its use in altering the degree of membrane-lipid unsath.
L24 AMSWER 11 OF 19 HOAPIUS COPYRIGHT 1997 ACS
1994:007537 | Issument No. 121:097399 | Altering the linclenic and
     limpleid adia content of plant pils by altering the levels of
     Innoleic wold desaturase. Gibson, Susan Irma; Kishore, Banesh
Murthy; Buff, Thomas Gene; Somerville, Christopher Roland; Arondel,
     Vindent Swan-Marie Armel Monsanto Co., USA; Michigan State
     University). ECT Int. Appli WO 9418337 Al 940818, 143 pp. DESIGNATED STATES: W: CA, TP, TS, US, EW: AT, BE, CH, DE, DK, ES, FR, CB, GE, IE, IT, DU, NO, NO, PT, SE. (English). CODEN: PIXXD2.
     APPLICATION: WE 94-US1821 MC204. PRIORITY: US 98-14431 980205; US
     **:-11**:51 9:31122.
     The lincheric acid content of vegetable oils is altered by changing
ΑВ
     the levels of expression of linoleid acid desaturase, e.g. by
     expression of a heterologius gene or antisense gene for the enzyme.
     A cDMA for the enzyme derived from the fad3 game of Brassica napus
     was introduced into wild-type and fadD mutants of
     Arabidipsis thaliana by Aurobapterium-mediated transformation and
     transferit plants prepd. Transformation of the wild type increased
     the linch-mate content form 31.9.4-.4.5 to 51.5.4-.10.9 molf of
     fatty acids and in the fall mutants the
     undrease was from 6.7.+-...? to 48.1.+-.15.5 molt of fatty
     acids.
     TOM 01.3N 115-32
IC
     CC
     11-1 Blant Birchemistry
     Shotikh ordss-referencekk : 3
ST
     Timoleate desaturase plant linolaid acid level
ΙT
     Adabidgesis thaliana
        (fig) were of; alteria; the limplemic and limpleid acid content
        or plant cils by altering the levels of linoleic acid desaturase)
ΙT
     Gene, plant
     EL: Block (Billiginal study)
        (tadi, for limileate downturase of Brassica mapus; altering the
        limitanic and limbleic acid content of plant oils by altering the
        levels of limbleid and desaturase)
     Gene, plant
T T
     PL: BELL Fieldgical at My
        (1350, of Arabidopsis thaltana; altering the limitenic and
        limiters adid dontent of plant bils by altering the levels of
        limilard adid desaturabe)
TΤ
     Gene, plant
     EL: BIBL Bibligical study
        (tadD, for limpleate desaturase of Arabidopsis thallaha; altering
        the linchenic and limbleid acid content of plant oils by altering
        the levels of linoleic acid desaturase)
ĽΤ
     Gene, plant
     EL: BIDL (Biblogical study)
        tfadE, for lincleate desaturase of Arabidopsis thallana; altering
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the linolenic and linoleic acid content of plant oils by altering
        the levels of limpleid acid desaturase
     Protoin sequences
ΙT
        (of lineleic acid desaturases of Arabidopsis and Brassica)
ΙT
     Plasmid and Episome
        (pMON13801, pMON13803, expression vectors for plants; altering
        the linclenist and limpleid adid content of plant bils by altering
        the levels of lincless acid desaturase:
     Plasmid and Episones
ΙT
        (jMNN19914, jMON19909, Brassida napus lincleate desaturase
        antisense gene on; altering the limplemic and limpleic acid
        content of plant oils by altering the levels of linoleic acid
        desaturase)
ΙT
     Plasmid and Episome
        q-TiDESS, Brassida mapus linoleate desaturase gene on; altering
        the limelenis and luncheid addd content of plant oils by altering
        the levels of lincheld acid desaturase
ΙT
     Plasmid and Episome
        qTiDEST, lincleate desaturase dene of Arabidopsis thaliana on;
        altering the limblemic and limbleic acid content of plant oils by
        altering the levels of lincleic acid desaturase)
TΤ
     F:1 ar.*
    Fape plant)
     Seed
     Soykman.
        of ranscanic; altering the limplenic and limpleic acid content of
        plant oils by altering the levels of limbleid adid desiturase).
     Flant stress
ΙT
        foold, improved resustance to; altering the linolenic and
        luncheid adia content of plant oils by altering the levels of
        lincleic acid desaturase)
ΙT
     Leoxyribonuolei: adid meguendes
        (complementary, fir limilets abid desaturases of Arabidopsis and
        Brassidar
     Leamyribanualeic saids
IΤ
     EL: ÁTT (Biblog: sai use, unclassified); BIOL (Biblogical study);
     USES Treat
        (complementary, antisense, to fad3 gene for linoleate desaturase
        :: Arabidops:a thalwana; altering the windlenic and lincleic acid
        centent of plant fils by altering the levels of linolete acid
        desaturase)
ΙT
    Midroorganism
        qhytopathogenic, improved resistance to; altering the Linolenic
        and limeleic acid content of plant bill by altering the levels of
     lineleic abid desaturase)
Fats and Glyperidic bils
     FL: PMF (Bioindustrial manufacture); PRP Properties); BIOG
     (Biological study); EEEP (Preparation)
        (regetable, altering the linelenic and lineleic acid content of
        plant oils by altering the levels of linoleic acid desaturase).
Ţm
     112-x1-1, 9-Octadecencic acid (2)-, biological studies
     Finolenic acid 3052-06-0, Linoleic acid desaturase
     EL: AGR (Agricultural use); MEM (Metaboli: formation); BIOL
     (Biological study): FORM (Formation, compreparative): USES (Uses)
         Saltering the limblenic and limbleic acid content of plant oils
        by altering the levels of limbleid adid desaturase)
ΙΤ
     148814-49-7 149955-97-5 158651-91-3
     EL: AGE (Agricultural use); PRP (Properties); BIOL (Biological
     study); USES (Uses)
        pamino abid sequence; altering the linelenic and lineleic acid
        menters of plant cils by altering the levels of linoleic acid
        dessturase)
     7142'-(4-8, .DELTA.15 Desaturase
IT
     EL: AGE (Agricultural ase); BOC (Biological occurrence); PRP
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(Properties); BIOL (Biological study); OCCU (Occurrence); USES
        scloning of Arabidopsis thalians gene for; altering the linolenic
        an: limiteic acid content of plant oils by altering the levels of
        fineleic acid desaturase)
     15 x 3/-3/-9 1592/3-33-0 1592(3-39-1
ΙT
     EL: AGE (Adricultural use); PEP (Properties); BIOL (Biological
     study,; TSES (Uses,
        'hurl-otide sequence; alt-rind the linelenic and lineleic acid
        content of plant oils by altering the levels of linoleid acid
        deraturase)
L24 ANOWER 12 OF 19 HOWERUS CONTRICHT 1997 ACS
1994:626646 Discument No. 121:124646 Molecular cloning of dDNA for
     mi uncachal delta-12 fatty acid
     desaturases and their use for molepular breeding of plants.
     Lightner, Jonathan Edward; )Obuley, John Joseph (du Pont de Nemours,
     E. I., and Co., USAG: POT Int. App). WO 411518 A1 340526, 147 pp.
     DELIGNATED STATES: W: AU, BE, CA, CR, DS; FW: AT, BE, CH, DE, DK,
     ES, PA, GB, GR, IE, IT, LU, IM, ML, PT, SE. (English). CODEN:
     ENDMOG. APPLICATION: WO 3:-M39987 981018. PRIORITY: US 92-977889
     921117.
    The prepr. and use of nucleic abid fragments encoding fatty
ΑВ
     acid desaturases and related ensymes are
     described. The invention permits alteration of plant liped composi-
     Chineric genes incorporating such nucleic acid fragments with
     surrable regulatory sequences may be used to preate transgenic
     plants with altered levels of unsatd. fatty acids. The ploning of
     cDNA for fatty acid .DELTA.12
     -desaturases (pdeogl-OcA desaturases) from Arabidopsis
     theliana, Brassida napus, Glycine max, Zea mays, and Ricinus communic was demonstrated. The expression/of antisense Glymax
     fatty acid .DELTA.12-
     desaturase cDNA in soybeans to reduce the expression of the
     encyme in developing scybean seeds and use of the cDNA sequences for
     restriction fragment length polymorphism. RFLP) mapping was also
     demonstrated.
    ICM 014N018-53
IC
     ICC 0120016-88; 0018001-0 ; 0120001-68; A01H005-00
     11-1 (Elant Biochemistry)
     Section pross-reference(s): z_{\star} 17
     plant fatty acid desaturase \text{SDA}
     oloning; breeding lipid compn transgenic plant
     Plant breeding and selection
TΤ
        icloming of fatty acid desaturase
        WINA in relation to)
ΙT
     Cancla
     Solyme an
        ·fatty acid desaturase expression
        in, antisense diMA for redn. of:
ΙT
     Profein sequences
        "of plant midrosomal fatty acid
      desaturases)
ΙT
     Plasmad and Episome
         puph seals, pZ0seals, p2K sed2R, fatty acid
      desaturase antisense cDNA of Brassica napus on, for
        expression redn.)
ΤT
     Pats and Olyperidic bils
     RL: PEP 'Properties)
        (tran genic plant cells having altered level of, cloning of
      fatty acid desaturase in relation to)
ΤT
     Plant
        stranggenic, unsatd. fatty acid level regulation in, cloning of
        cDNA for fatty acid desaturase in
```

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relation to)
    Deoxyribonubleid adid sequences
        (samplementary, for plant microsomal fatty acid
      desaturases)
ΙT
     Deckyriborusleis asids
     FL: BIOL (Biological study)
        complementary, antisense, for fatty acid
      desaturase, for reducing desaturase gene
        empression in transgense plants)
ΙΤ
     Elasmia and Episome
        pSTII, fatty acid desaturase
        antisense cDMA of Glycine max on, for expression redn.)
     Genetic bolymorphism
TT
        restriction fragment Length, Genetic mapping, of gene for
      fatty acid desaturase of plants,
        sleading of fatty acid desaturase
        STONA in relation to)
     Farty acids, biological studies
     FL: PRP (Properties)
        funsatd., transgenic plant bells having altered level of, cloning
       of fatty acid desaturase in
        relation to:
     158283-24-0, .delta.-12 Fatty
TΤ
     acid desaturase (Arabidopolis thaliana clone
     p9.113) 158283-26-2, .delta.-12
     Fatty acid desaturase (Prassica napus
     clone pCF2-1650) 158283-28-4, .delta.-12
     Fatty acid desaturase (Glycine max clone
     Fatty acid desaturase (Zea mays clone
     pFadl#1) 158283-32-0, .delta.-12
     Fatty acid desaturase (Ricinus communis
     clone pRF2-10) 158283-34-2, .delta.-12
     Fatty acid desaturase (Ricinus communis
     close pRF1970-42)
     FL: BIOL (Biological study)
        (amino acid sequence is and cloning of cDNA for, mol. breeding in
        relation to:
     77 % - Fi-F. Hatty acid .DELTA.12-hydroxylase
ŢΤ
     FL: FICE (Bithedical study)
        Grene for, method for cloning of)
     8440.19-91-9
ΙT
     FL: BICL (Biological stody)
     (gene for, of plants, method for bloning of)
154.53-33-3, DNA (Arabidopsis thalians blone pAGF2-6 .delta.
ΙΤ
     -12 fatty acid desaturase
     aer.e.
     FL: BIGL (Biblogical study); PRP (Propert.es)
        nuclectide sequence and cloning of:
ΙT
     15. NC-16-7, DMA (Arabidopsis thaliana clone p92103 .delta.
     -12 fatty acid desaturase
     cDMA and flanks) 158288-25-1, DMA (Bras.ica napus clone pCF2-165D
     fatty acid desaturase cDNA and flanks)
     15-3-3-27-3, DMA (Glydine max dlone p3F2-163K .delta.-
     12 fatty acid desaturase < ONA
     and :larks) 198283-29-8, DNA (Zea mays offene pEad2#1
     .delta.-12 fatty acid
     desaturase cDNA and flanks) 158233-31-9, DNA (Ricinus
     communis clone pRF2-10 .delta.-12 fatty
     acid desaturase cDNA and flanks) 158283-53-1,
     DNA (Ricinus communis clone pRF1970-42 .delta.-12
     fatty acid desaturase SDNA and flanks)
     RL: BIBL Biological study); PRP (Properties)
        (nucleatide sequence and cloning of, mol. broading in relation
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to)
TT
     141-12-7, Eicinoleic acid
     FL: PEP (Properties)
        (transgenic plant cells having altered level of, cloning of
      fatty acid desaturase in relation to)
L24 ANSWER 13 OF 19 HOAPLUS COPYRIGHT 1997 ACS
1994:63498L Dicument No. 121:324+53 Arabiappaid FAD2 gene encodes the
     ensyme that is essential for polyunsaturated lipid synthesis.
     Cauley, John; Lighther, Johathan; Feldmann, Henneth; Yaday,
     Marenira; Bark, Ellen; Browse, John (Inst. Bool. Chem., Washington
     State Univ., Pullman, WA, 391/4-6340, USA . Plant Cell, 6 1),
     147-59 (English) 1994. CODEM: PICEEW. 133N: 1040-4631.
AΒ
     The polyunsatd, fatty acids limoleate and .alpha.-limolenate are
     immortant membrane components and are the essential fatty acids of
     human nurrition. The major ensyme responsible for the synthesis of
     these compass is the plant pleate desaturase of the endoplusmic
     reticulum, and its activity as controlled in Anabidopsis by the
     fatty acid desath. . (fad. librus. A
     fad. allele was identified in a population of Arabidopsis on which
    .mutations had been oreated by T-DMA insertions. Genomic DNA
     fQ and in the T-DNA was bloked by plasmid rescue and used to isolate
     cDNA this genomic closes of FADE. A cDNA contg. the entire FADE
     roding sequence was expressed in faci mutant plants and
     shown to remplement the mutant factly acid phenotype. The
     occuped amini abia sequence from the cDMA showed homel, to other
     plant desaturases, and this confirmed that FAD2 is the structural
     gene for the desaturase. Get blot analyses of FAD2 mENA levels
     showed that the gene is expressed throughout the plant and suggest
     that transcript levels are in excess of the amt, needed to account
     for cleave desath. Jequence anal. identified histidine-rich motifs
     that could contribute to an eron binging site in the cytoplasmic
     domain of the protein. Such a position would facilitate interaction between the desaturage and byth chrome b\bar{t}, which is the direct source of electrins for the desath, reaction, but would limit interaction
     of the active site with the fatty acyl substrate. Figures:
CC
     Section or ass-reference(s : )
     gene PAD. pleate desuturase complende Arabidopsis; cDNA FAD. oleate
ST
     desaturase seguende Arabidopois
ΙT
     Arabicorsis thalland
        Arabadopsis BADU gene for obeate desaturase that is essential
        for polymnsatd. Lipid synthesis)
ΙT
     Cene, plant
     FI: BIOL (Biological study
        'PADU; Arabidopsi: PADU gene for cleate desaturase that is
        waserfial for polyunsato. Lipid synthesis:
ΙT
     Leckyrikomusleis acud sequences
        +of Amaricopsis FAD2 game for oleate desaturase)
ΙT
     Engine minotional sines
     Pritein sequences
         or Arabidopsis PAD2 pleate desaturase
T
     894 9-30-1, Oleane desaturase
     EL: BAC (Biological activity or effector, except adverse); PRP
     (Properties); BIOL (Biological Study)
        (Arapidopsis FADU dene for oleate desaturase that is espential
        for polyunsatd. Lipid synthesis)
IΤ
     158283-24-0, Oleate Gesaturase Arabidopsis thaliana clone
     pFla seno FAD2)
     EL: PEP Properties:
        (amin) acid sequence; Arab:dopsis FAD2 gene for oleate desaturase
        that is assential for polymsatd. lipid synthesis)
ΙT
     15241 - 16-7
     FL: PRP Properties)
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(nucleotide sequence; Arabidopsis PAD) gene for cleate desaturase that is essential for polyunsatd. lipid synthesis) L24 ANSWER 14 OF 19 HCAPLUS COPYRIGHT 1997 ACS 1994:474800 Dominant No. 121:74800 Identification of conserved domains in the .DELTA.12 desaturases of dyanobacteria. Sakameto, Teshie; Wada, Hajime; Mishida, Ikue; Ohmori, Masayuki; Murata, Morro (Dep. Mol. Bromechan., D.iv. Advanced Studies, Okazaki, 444, Japan). Plant Med. Bacl., .4(4), 648-50 (English) 1994, CODEN: PMBIDB. ISSN: 0107-441... AΒ Cyanobacterial genes for encymes that desaturate fatty acids at the .DELTA.12 position, designated desA, were isolated from Symechodystis ECC6714, Symephococous POC7002 and Anabasma variabilis by cross-hybridization with a DMA probe derived from the desA dene of Symechodystis FCC6:03. The genes of Symuchomystis PCC6/14, Symechococcus PCC7002 and A. variabilis encode proteins of 349, 345 and 360 amino acid residues, rusp. The transformation of Symechologus PCC7942 with the desA genes from Symetholystis FCCv714, Symethodocous FCC7602 and A. variabilis was assled, with the ability to introduce a second wingble bond at the .DELTA.12 position of fatty actids. The amine acid sequence of the products of the dosA genes rowealed the presence of four conserved domains. Since one of the conserved domains was also found in the amine acid sequences of .imeda.l desaturases if Brassina napus and mund bean, this domain may play an essential role in the introduction of a double bond into tatty acids bound to membrane lipids. R-R (Figherical Genetics) CC Jection pross-reference(s): 7, 11 desaturase dene desA sequence oyansha teria; Anahaena Synechopodous ST Dynach coystis desaturase gene sequence Amabaena variabilis ΙT (desaturase gene desA of, updated midlotide sequence of) ΙΤ Dyrac chicago cous Byta chroystas (dene desA of, nucleotide and encoded reptide sequences of) ΙT Depayribonucleic abid sequences ouf desaturase dene desA, or Symechopystis and Symechoppous; ΙТ Eridein sequences (of desaturase, of Symethorystis and Symethococcus) ΙT Gere, microbial El: BIOL (Biological study) idesA, for desaturase, of Symeothogystis and Symeothogocous, nurlectide and encoded poptious sogninous of ΤT 156532-35-3, Delta 12 desaturas . Syncahorystis ECC(714) 156532-36-4, Delta 12 desaturase (Symeone cooccus ECO700) . Hi: PEE (Enoperties) (uning adid sequence of: 198462-28-8 188462-09-6 198971-60-5 ΙΊ BL: BIOL (Biblogical study); PEN (Englerthes) inualectide sequence of: L24 ANDWES 10 OF 19 HOMPING COPYRIGHT 1:17 ACS 1994:184.75 Do ument No. 120:184.15 A gene end ding a dhloroplast . hera. - r fatty acid desaturase complements alterations in fatty acid desaturation and onloroplast copy number of the fad? mutant of Arabidopsis thaliana. Iba, Hoh; Gobson, Sue; Mishruon:, Takumi; Fure, Takuichi; Michimura, Mitsuo; Ar mdel, Vincent; Hugly, Sudanne; Someordelle, Chris (Fab. Spi., Kyushu Univ., Eukubka, 81d, Japan). T. Biol. Chem., 26 (3.), 34099-105 (English) 1995. CODEN: USCHA3. ISSN: 1981-9855.

Mutations at the fad7 locus of A. thalian: (previously

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AB

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called fadD) cause decreased desatn. of dienoid
fatty acids in ohloroplas' lipids in plants grown
at elevated temps. This suggested that the Tad7 locus encodes a
chloroplast .cmega.-3 desaturase that datalyces the desatn. of
lipid-linked 18:2 and 16:3 fatty acids. In order to clone the fad?
gene, it was first genetically mapped relative to the flanking RFLP
markers 4547 and 2438A on enromosome 3, and yeast artificial
chromosomes covering the locus were identified. A putative
desaturase cDMA clone that was isolated by low stringency
heterologous probing with a cDNA for an endoplasmic
reticulum-localized .omeg..-3 desaturase .fai3) hybridized to the
yeast artificial phromosomes and bould not by resolved from the locus by ESTLP mapping. Expression of the bDNA in transgenic fad7 \,
mutant plants resulted in restoration of wild-type fatty
actic compon. and suppression of a previously obsd. effect of the fad7
mutation in chloroplast no. indicating genetic
complementation. The structural gene contained seven introns within
a booting sequence of 1998 base pairs, which empodes a 446-amino acid
polypeptide of 51,172 daltons. The N-terminal region of the fad7
gene product contained a schsensus chloroplast transit peptide.
Except for the N-terminal domain, the deduced amino acid sequence of
the fact gene product had high homol, to the fact gene product,
indicating that fad7 encodes an .omega.-3 desaturase and that the
two genes arcse from a common ancestral gene. There was no apparent
effect of growth temp. on the steady-state levels of fad7 mRNA in
wild-type plants.
3-3 (Biochemical Genetics
Seption pross-reference(s : 7, 11
fatty acid desaturase gener sequence
Anabidopsis; mapping sequence gene fact Arabidopsis
Arabidopsis thaliana
   (fatty acid desaturase gene fad7
   of, isolation and sequence and mapping of
Chleroplast
   fatty acid desaturase of,
   Arabidopsis thaliana game for, isolation and sequence and mapping
Decayribonucleic acid sequences
   of fatty acid desaturase gene
   fad7, of Arabidopsis thaliana)
Erotein sequences
   of fatty acid desaturase, of
   Arabidepsis thaliana)
Genetic mapping
   oof fatty desaturase gome fad7, on Arabidopsis thaliana
   chromosome i)
Gene, mlant
EL: BIOL (Biclodical study)
   efact, for fatty acid desaturase,
   of Arabidopsis thaliana, isolation and sequence and mapping of)
Chromesome
   Arabiaopsis thaliana :, fatty acid
 desaturase gene fau7 mapping)
Peptidos, biological studies
EL: BIOL Biological study)
   transit, in fatty acid desaturase,
   of Arabidopsis thaliana
149955-97-5, .omega.-3-Fatty acid
desaturase (Arabidopsis thaliana clone g4)
FL: PEP (Properties)
    amino abid sequence of)
153608-91-4, Ger.Bank S66769
LL: PEP (Properties)
   inucleatide sequence of and mapping of:
                       KATHLEEN FULLER BT/LIBRARY 308-4290
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L24 AMSWER 16 OF 19 HCAPLUS COPYRIGHT 1997 ACS
1994:47043 Decrument No. 120:47 (4% Cloning of nigher plant .omega.-3 fatty acid desaturases. Yadaw, Narendra
     S.; Wierzbicki, Anna; Aegerter, Mary; Caster, Cheryl S.; Berez-Grau,
     Duis; Finney, Anthony I.; Hitz, William D.; Booth, J. Russell, Jr.; Schweiger, Bruce; et al. 'Exp. Stn., E. I. duPont de Nemburs and
     Co., Wilmington, DE, 19880-0402, USA). Plant Physiol., 108(2), 467-76 (English) 1998. (ODEN: PLPHAY. ISSN: 0022-1889.
AΒ
     Arabidipsis thaliana T-DNA 'nunsformants were scheened for
     mutations affecting seed fatty acid compn. A mutant
     time was found with reduced levels of limitenic acid (18:3) due to a
     T-DMA insertion. Genomic DMA flanking the T-DMA insortion was used
     to obtain an Arabidopsis of DNA that encodes a polypeptide identified
     as a microsomal .omega.-  fatty acid
     desaturase by its complementation of the mutation.
     Anal. of ligid content in transgenic tissues demonstrated that this
     enzyme is limiting for 18:3 prodn. in Arabidopsis seeds and carrot
     hairy rocts. This CDNA was ared to isolate a related Arabidopsis
     cDNA, whose mBNA is accumulated to a much higher level in leaf
     tissue relative to root tissue. This related cDNA encodes a protein
     that is a nomelog of the mixesomal desaturase but has an N-terminal
     extension deduced to be a transit peptide, and its gene maps to a
     position consistent with that of the Arabidopsis fadD locus, which
     controls plasted .cmega.-% dewath. These Arabidopsis cDNAs were
     used as hybridization probe: to isplate dDNAs encoding homologous
     proteins from developing seeds of scybean and rapeseed. The high
     degree of sequence similarity between these sequences suggests that
     the .:mega.-3 desaturase: use a common enzyme mechanism.
     3-3 (Bischemical Genetion)
     Section pross-reference(s): 7, 11
     sequence plant fatty acid desaturase
     gene; Arabidopsis fatty acid desaturase
     yene fact; soybean fatty acid desaturase
     gene (adD; rapeseed fatty acid
     desaturase gene facil
ŤΨ
     Gene, plant
     RL: BICL (Biological study)
         fad?, for fatty acid desaturase of
        Arabidopsis and scybear and rapeseed, sequence of)
ΙT
     Arabidipsis thaliana
     Brazeles napus
     3 mylear
         fatty acid desaturases of
        microsomes and chloroplast of, sequence of genes for)
         Hinchenic acid level: in Arabidopsis thaliana, bloming of
      fatty acid desaturase gene affecting)
IT
     Epotein sequences
        of fatty acid desaturase, of
        veyhear and hapeseed and Anabidopsis microsome and chloroplast)
     Decorymiconucleid adid sequences
          implementary, for fatty acid
      desaturase, of soybean and rapeseed and Arabidopsis
        minrosome and onlonoplist)
IT
     Bene, plant
     RL: BIOL (Biological study)
         feath, for fatty acid desaturase of
        Arabidopsis and soybean and rapeseed chloroplast, sequence of)
     465-40-1, Linolenia acid
     EL: PEP (Properties)
        (Arabidopsis thaliana leeds with reduced levels of, bloning of
      fatty acid desaturase gene causing)
IΤ
     149955-96-4, .omega.-5 Fatty acid
                            KATHLEEN FULLER BT/LIBEARY 308-4290
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desaturase (Arabidopsis thaliana clone CF1 gene fad3)
     149955-97-5, .omega.-? Fatty acid
     desaturase (Arabidopsis thaliana chloroplast clone CFD gene
     fadD precursor) 149956-00-3, .omega.-3 Fatty
     acid desaturase (Glypine max plone GM3 gene fad3)
     149956-01-4, .omega.-? Fatty acid
     desaturase (Glyrine max biloroplast rline GMD gene facD)
     152208-01-0, .omega.-: Fatty acid
     desaturase (Brassica napus chloroplast clone BND gene :adD
     precursor) 152208-02-1, .omega.-3 Fatty
     acid desaturase (Brassica napus clone BM2 gene
     fad:
     EL: PEP (Properties)
        (amino acid sequence of)
     149915-89-5
                   149955-90-3
                                   149955-92-0
                                                 149958-93-1 151497-59-5
     151497-60-3
     RL: BIOL (Biological study); PRP (Properties)
        (nucleotide sequence ci)
L24 ANSWEE 17 OF 19 HCAPLUS COPYRIGHT 1997 ACS
1993:818639 Document No. 119:218623 Map-based cloning of a gene
     controlling omega-8 fatty acid
     desaturation in Arabidopsus. Arondel, Vincent; Lemieum,
     Bertrand; Hwang, Inhwan; Gibson, Sue; Goodman, Howard M.;
     Somerville, Chris R. (Plant Res. Lab., Michigan State Univ., East
Lansing, MI, 48824-1812, USA). Science (Washington, D. C., 1885-),
     258(508(), 1858-5 (English: 1880. | CODEM: SCIEAS. | ISSN: 0036-8075.
AΒ
    A gene from the flowering plant Arabidopsis thaliana that encodes an
     .pmeda.B desaturase was cloned on the basis of the genetic map
     position of a mutation affecting membrane and storage
     liptd fatty sold compo. Yeast artificial chromosomes covering the
     genetic locus were identified and used to probe a Brassica napus seed rONA library. A B. napus rONA clone for the desaturase was
     identified and introduced into roots of both wild-type and mutant A. thaliana plants by Ti plasmid-mediated
     transformation. Transgenuc tissues of both mutant and
     wild-type plants had significantly increased amts. of the
     fatty acid produced by this desaturase.
CC
     3-3 (Biochemical Genetics,
     Seption pross-reference(s : 1, 11
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     cmeda? desaturase gene mapping Arabidobsis; cDNA omega: desaturase
     sequence cloning Brassida
ΙT
     Arabiacesis thalians
        tgene facilifix .imega.s lincleate desaturase of, mapping of)
ΙΤ
     Genetic mapping
        (of gene faul for .omega.: Linoleate desaturase, of Arabidopsis
        thaliana)
ΙT
     Erotein seguences
        fof .omega.E lincleate deservrase, of Brassida napus)
ΤT
        (transformation of, of Arabixopsis thaliana, by .omega.3
        linoleate desaturase cDNA of Brassica napus)
ΙT
     Brassida napus
        (.tmega.) lincleate desaturase cDNA of, sequence and cloning in
        Arabidopsis thaliana off
ΙT
     Gene, plant
     EL: BIOL (Biological study)
        (fadf, for .omega.5 linoleate desaturase, of Arabidopsis
        thaliana, mapping and complementation of)
ΙT
     Deoxyribonucleid abid sequences
          complementary, for .omega.U linbleate desaturase, of Brassica
        napus)
ΙT.
     Transformation, denetic
        {transgenosis, of Arabidopsis thaliana roots, by .omega.3
                             KATHLEEN FULLER BT/LIBRARY 308-4290
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lingleate desaturase oDNA of Brassica mapus)
ΙT
     Chromosome
         Arabidopsis thaliana 2, gene fad? for .omega.3 linoleate
         desaturase mapping on)
     148814-49-7
ΙT
     RL: BAC (Biological activity or effector, except adverse); PRF
     (Properties); BIOL (Bibliogudal study)
        (amino adia sequence of, complete)
     27213-43-6
ΙT
     BL: FORM (Formation, nonpreparative)
        -formation of, by transgenic Arabidopsis thaliana expressing
        Brassica napus .omega.3 linoleate desaturase cDNA)
     145/10-76-8, GenBank L01418
ΙT
     RL: BIOL (Biological study); ERP (Properties)
        inuclectide sequence of,
L24 ANSWER 15 OF 15 HUASLUS CORYRIGHT 1997 AGS
1993:653376 | Document No. 119:16676 | Fatty acid
     desaturase genes from plants and their use in altering fatty
     adri composition of plant pils. <u>Browse, John; Grau, Luis Perez;</u>
Finney, Anthony J.; Pierce, John W., Jr.; Wierzbicki, Anna M.;
     Waltav, Mirendra S. (du Bont de Nemburs, E. I., and Co., USA). PCT
     Int. Appl. WO 9311245 Al 980610, 167 pp. DESIGNATED STATES: W: AU,
     BR, CA, TP, RU, CA, CS; FW: AI, BE, CH, DE, DK, ES, FR, GB, GR, IE,
     IT, LU, MI, NL, ST, SE. (English . CODEN: PIXXD2. APPLICATION: WO RE-US16.-4 921203. PERORITY: US 91-814289 911214.
     Elastid and microsomal delta-15 desaturase cDNAs
AВ
     of Arabidopsis thaliana, Brassida napus, and Glydine max are cloned
     and sequenced. The effect on 18:2 and 18:3 content of expression of
     antisense delta-15 desaturase cDMA in B. napus
     and G. max was examd. Use of the cloned cDNA for RFLP anal. and
     plant breeding was explored.
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     TCM C1/NO15-53
     TG3 | G10N015-88; G118001-10; G180001-88
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     3-3 (Bit themical Genetical
     Section Pross-reference(s): 11, 17
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     fatty acid desaturase offia plant
     sequence; Arabidopsis deltali desaturase oDNA sequence; Brassica
     delta19 desaturase cDNA sequence; Glycine delta15 desaturase cDNA
     requence; cil glyceridic plant unsato fatty acid; EFLP plant
     bremaing desaturase cDNA
ΙT
     Elant breeding and selection
         RELF anal. in, plant .DELTA.-15
      fatty acid/glyserolipid desaturase
        CONA : br)
     Gene, plant
ΙT
     RL: BIOh (Billogical Study)
        if or .DELTA.-15 fatty acid
         gly-brolipid desaturase of Arabidopsis thaliana and
        Brassida napus and Blydine max
IΤ
     Erotein dequences
        : of .DELTA.-15 fatty acid
         gly > rolipid desaturase of Arabidopsis thaliana and
        Brasside napus and Blydine max-
     Flant
        foil-producing, alteration of Linclenia acid content of
        transgeric, cloning of plant .DELTA.-15
        Hesaturase oDNA in relation to)
     Arabid:psis thaliana
     Bransica napus
     Codos (Theobroma dadao)
     Corn
     Motton
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Safflower
     Cowbean
     Sunflower
         /plant .DELTA.=15 fatty
      acid glycerolipid desaturase cDNA expression
        in, for alteration of linolence acid content of oil)
     Mar. and Glymeridic bils
     FL: BIDL (Bidlogical study)
         (with altered limblehic acid content, transgenic plants
        producing, cloning of plant .DELTA.-15 desatinase cDNA in relation to:
     Decomyricanu deid adid sequende
         coemplementary, for .DELTA.-15 fatty
      acid/glyperalipid desaturase of Arabidopsis
        thaliana and Brassida hapus and (Hydine mam)
ΙT
     Genetic polymorphism
         Trestriction fragment length, of glant genomes, plant
      .DELTA.-15 fatty acid
         glysemalipid desaturase aDMA for anal. of:
     149955-96-4, .DELTA.-15 Denaturase
ΙT
     Arabitopsis thaliana of me pCP3: 149955-97-5,
     .DELTA.-15 Fatty acid
     desaturase (Arakidopsis inaliana of me pACER-1 plastid)
     149955-98-6, .DELTA.-15 Glycerolipia
     desaturase (Prassica napus clone pBNSF3-2 microsomal)
     149955-99-7, .DELTA.-15 Glyderulipid
     desaturase (Brassica napus clone pBMSFd-2 plastid)
     149956-00-3, .DELTA.-15 Desaturase
     (Glycine max clone pKF1 migrosomal) 149956-01-4,
     .DELTA.-15 Desaturase (@)y-fine max dine
     pSFU-1183-wp plastid) 149956-02-5, .DELTA.-
     15 Desaturase fragment (Sea mays clone pECREO,
     149956-03-6, .DELTA.-15 Decaturace
     fracment (Arabidopsis theleans clone pFack-2 plastid)
     FL: PEP (Properties)
        camino abid sequence
     14 * (55-8 :- 3, DMR (Arabid pris thalians clone pCF3 .DELTA.-
İΤ
     15 desatrinase oDNA and flanks) 14 (9:5-9:-3, DNA
     (Arabidopsis thaliana of me pACEU-2 plastic fatty
     acid .DELTA.-15 desaturase
     cDMA and flunks) 149985-41-3, INA (Brassica napus clone pBNSF3-2
     microsomul .DELTA.-15 glypero.:pud desaturase cDNA and flanks) 14995 - 82-1, ENA (Glycine max clone pXF)
     microsemal .DELTA.-15 departurase oDMA and
     flanks) 149955-98-1, DNA (Grycine max clone pSFD-118bwp plastid
     .DELTA.-15 desaturase cDNA and flanks)
     14:056-94-2, INA (Zea mays plone pP 000) .DELTA.-15 denaturale \text{MINA})=14.995-000 . DNA (Arabidopris thaliana clone
     pFacemes plastic .DELTA.-15 desaturace cDNA)
     EL: BIOL (Enclosidal study,; PEF (Properties)
         involvotice sequence if, use in REWP anal. and in transgenic
        plants for alteration of farty and content of oils of)
     46 -46-1. Linelania acid
ΙT
     ELE: PEP (Properties)
          tran.denic plants producing oil. with altered levels of, cloning
        of plant .DELTA.-15 desaturase cDNA in
        relation to:
L24 ANIWER 1: OF 19 HOAFLUS COPYRIGHT 1997 ACS
1991:18174 Obsument No. 114:1-574 The OLE1 dene of Saccharomyces
     cerevisiae encodes the .DELTA.9 fatty acid
     desaturase and can be functionally replaced by the rat
     stearcyl-CcA desaturase jene. Stukey, Joseph E.; McDonough,
Virginia M.; Martin, Charles E. (Nelson Biol. Lab., Rutgers, State
                             HATHLEEN FULLER BT/LIBRARY 308-4290
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Univ., Picsataway, NJ, (9355-1059, USA). C. Biol. Chem., 265(33),
     20144-0 (English) 1990. CODEN: JBCHA3. ISSN: 0021-9258.
     Strains of S. derevisiae bearing the olel mutation are
AB
     sefective in unsatd. Satty actd (UFA) synthesis and require UFAs for
     growth. A previously isolated yeast denomic fragment complementing
     the old! mutation was sequenced and dotd, to encode the
     .DELTA.9 fatty acid desaturase encyme
     by companison of primary amin: acid sequence to the rat liver
     she royl-CoA desaturake. The OLET structural gene encodes a protein
     of 310 amino acids (201 hydrophobid) having an approx. mol. mass of
     10.4 kDa. A U57-amin) addid internal region of the yeast open
     reading frame aligns with and shows 30% identity and 60% similarity
     to the rat liver stearcyl-CoA desaturise protein. This comparison
     disclored 3 enort regions of high convergive amino acid identity
     \ell(3n) ) including one 11 of 12 perfect residue match. The predicted
     yeast engyme contains .dtpred.4 potential membrane-spanning regions
     and several shorter hydrophobic regions that aligh exactly with
     simular sequences in the rat liver protein. An olel mene-disrupted
     yeart struin was transformed with a yeast-rat chimeric gene
     bond isting of the promoter region and N-terminal 27 domains of OLEI
     fused to the rat desaturase coding se pience. Pusion gene
     transformants displayed near equiv. Growth rates and modest lipid
     compa. changes relative to wild-type yeast control implying a
     significant conservation of JESTA.9 desaturase tertiary structure
     and efficient interaction between the rat desaturase and yeast
     gym with one bi.
     3-3 (Brownems hal Genetics)
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     Section obosa-reference(s): 7
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     fatty acid desaturase gene sequence
     Sadrharomydes; gene OLE1 seguende Sad tharomydes
     Sad haromydes demevisise
        (fatty acid desaturase gene GLE1
         f, nucleotide and enouded peptide sequences of)
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     Endiplasmid beticulum
        (fatty acid desaturase insertion.
        into call membrane of, of Saccharomyce, cerevisiae)
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     Erotein sequences
        fof fatty acid desaturase, of
     Japoharomynes ceremisiae, complete
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        oof transformed Sadohardmydes derevisiae contq. fatty
      acid desaturase dene
     Complementation, generic
        estearbyl CoA desaturase gene in, of yeast cells contg.
      mutant fatty acid desaturase
        in mess)
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         stear yl CcA desaturase game of, in complementation of
        Machinaromy nes deperisiae contg. mutant fatty
      acid desaturase denel
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     Tepmyr.bonucleir adid sequences
        Frowl NoA desaturase-specifying, of Sadonaromyces desevisiae,
        :om; lete)
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        emeati., of transformed Sapoharomyces cerevisiae contg.
      fatty acid desaturase gene)
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     Generald Genetic clament, microbial
     FL: BIOL (Bibliogical study)
        OLE1, for fatty acid desaturase,
        of Saczkar mydes derevisiae, nublebtide and encoded peptide
        Lequences of)
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ΙT
    131198-85-1
    FL: FFF (Properties)
        famino acid sequence of)
ΙT
     3014-34-0, .DELTA.9 Fatty acid
     desaturase
     FL: FF.P (Properties)
        gene for, of Maccharomyces cerevisiae, structure and
        complementation anal. of)
     181198-68-8, Deckyribonucleic acid (Saccharomydes cerevisiae gene
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    CLE1)
    RL: BIOL (Biological study); PRP (Properties)
     [Nucleotide sequence of) 
37-11-3, Fatty acid 16:0, biological studies 57-11-4, Octadecanoic
    acid, biological studies -112-80-1, 9-Octadecenoic acid (Z)-,
    kiological studies 373-43-9 544-63-8, Tetradecanoic acid,
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      acid desaturase denote
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     Desaturase, oleoyl obenzyme A (Petroselinum crispum clone ELI12)
       - POI) CA INDEM NAMED
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  Mil GenBank US6374-demand protein GF 2001792
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.E.N
      196217-80-8 REGISTRY
      384-721-Desaturase, bleate (Corvins avellana done I) (9CI) (CA
      INDEX NAME:
      PROTEIN SEQUENCE
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     338
         1 QECTLERSESY VVYDLSLAFL ETYTATSYFH IMPHELDYNA WSTYWALQGO
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     Desaturase, eleate (Corylur avellana flore NE gene FAD2-N) 9CI)
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     382
           1 MOAKSEMPAT NEEKEGETEL GEARETEREE TLOGLERAUP PROEGESILE
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          51 SERVICYTIS DARLEYYTAT CYFRILIBER, CYLAWSTYWA LQGCELTGVW
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          51 RSFJYLIMDI LIASCFYYVA TTYFPLLPHP LOTFAWPLYW ACOGCYLTGV
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151 LERDEYFYPK KKSDIKWYGK YHNNPLGRIV MUTVOFTLGW PLYLAFNYSG
        201 RPYDGGEACH FHRMARIYND RERLQIYISD AGILAYCYGL YRYAAMGGVA
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126 ANUWER 6 OF 10 REGISTRY COPYRIGHT 1597 ACS EM ^{\prime} 192889-79-5 REGISTRY
     Devaturase, :lenylle-ithin (Brassica napus strain Westar iscenzyme
     F) (9CI - (CA IMBEX NAME)
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         1 MOWOGROWYS ELUPROPTON INDUFFREE PROGERRAL PERCENTRIP
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     Delaturage, clecyll-cithin (Frassica napus clone IMC120 asoenzyme D)
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        101 RPYDGGFECH FHENAPIYND REELQIYISD AGILAYCYCL FEYAAGQGVA
        251 SHYGFYGYPL LIWNGFLYLI TYLQHTHPSL PHYDSSEWLW FEGALATYDR
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           1: 127:135034
1.6 ANSWER 5 OF 36 REGISTEY COPYRIGHT 1997 AGS FIT \frac{1}{3} 192889-75-1 REGISTRY
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        1 MGAGGEMOVO PRIMEREDIT INEMPORTER FINGELMMAI PRHOFMRSIE
        SI EMPSYLIMDI IJACCEYYMA TOYFFLIPHE ISYFAMELYW ACQGCVLTGV
       101 WVIAHEOOHE ARMEDOWLDE TOOLIFHSEL LVEYESWEYS HREHHENTOS
       151 LEBUEYFYPK FESTORWYCK YDDUPLGETY MDTYCETDGW PLYLAFDYSG
       301 EPYDGGERCH FHENAFIYND EERLOIVISD AGILAVOYGL FRYAAGQGVA
       LEI SINGEYGUPH LUNIGFINIH CYLOHTHESH PHYDSSEWLW FEGALATVDE
ECI DYGILHFUFH NITDIHVAHH EFUTMPHYHA MEATRAINFI LGEYYOFDGT
       551 PVVKAMWELA RECITVEPTE (GEREGYEWY MNEI
HITS AT: 143-109, 141-140, 316-33
ME Unappedified
(·:
    MAII
: F.
    CE
     STM Files: CA, CARLUE
               1 APPEARMORD IN FILE (A. 1967 TO DATE)
               1 REFERENCES IN FILE CAPACE (19.7 10 TATE)
REFERENCE 1: 1.7:131014
1836 ANSWER - OF SO FROITTEN COSTRUCTIONS ACC
     186208-06-0 REGISTER
     Devaturase, .DELTA. - Fatty acros P.chia angusta) (901) (CA INDEX
     NAJEE)
F.:
     PROTEIN SEQUENCE
SQL 451
                                                                              · (
SEQ
         1 MODESMITOVI ARELABIDOVA MALAHDRELH MEGLEQERIS EQEWIWENWE
        51 RHINWINFIL VLAVEFACLI SYMVELKUH TEUTAVILYO FOGISITAGY
       101 HRHWAHFAYD CHUPYKIFFA DEGASAYEGS IKEWGHQHEV HERYTDIERD
       151 PYDASECEWY CHMOWNLINE NEETKAFADI SELLCOWVUR VQHRHYLLLIM
       201 VZMAFLEDAV LUHYDENDEW GOFTYACILE ANTIQQATEC VESLAHWIGE
       231 QPFDOMETPE DHVLTALYTE GEGYHNERHE FEYDYSMALK WYQYDETKVV
       301 IYLLSHI'JLA YULHHESONA IDQ ILQQQQ HHUDEMHARL NWGPQLCELP
       351 VWDKSTFFER AREQUOLVII SGIMHDCANF LIBERGOQAL LEISFGRDAT
       401 MAFNGGYYAH SNAAHNLLAT MRYAVIKDOG ANGDTFDAGL RYLASKENKK
                            KATHLEEN FULLER BT/LIBRARY 308-4290
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451 E
HITS AT: 138-142, 275-279
MF Unspecified
    HALL
CI
: F
    1174
     ∷T∷ Fil∈s:
                 CA, CAPLUS, TOXLIT
               1 REPERENCES IN FILE CA (1967 TO DATE)
1 REPERENCES IN FILE CAPLUS (1967 TO DATE)
REFERENCE
          1: 116:1139)1
126 ANGWER 11 OF 66 REGISTRY COPYRIGHT 1997 ACS
E.N
     180583-92-0 REGISTRY
\.\
     Desaturase, lincleate (Borago officinalis (PII) (CA INDEX NAME)
     PROTEIN SEQUENCE
.`QL
    448
         1 MAAQEKKULI SDELENEDKE EDIWIGIQGK AYOVEDWUND HPGGSFPLKS
.:EQ
        51 LAGQENTOAF VAFHEASTWE NIDEFFTGYY LEDYSUSEUS EDYRELDFEF
       101 SEMGLYDEKG HIMFATLOFI AMLFAMSVYG VLECEGVLUH LESGOLMGFL
       191 WIQSGWIGHD AGHYMVVCDS ELDEFHGIFA ADGLEGISIG WWRWDHDAHH
                                                             = : = : : : : = : = :
       UGI TACMOLEYDE DUQYTPELVV SCREFGSLTC HEYERKLTED SLBEPFVSYQ
       .51 HWTFYPIMCA ARLDWYVQSU IMBLTERNYO YRAQEDLGCD VESIWYPDDV
       331 SCLPUMGERI MEVJASLOVI GMQQVQESIN HEYSSVYYGK PKGMIMFEKQ
       981 TDGTADICJE PRMOMEROGE OFQIEHHLEP KIKECALEKI SPYVILICKK
       411 HNLEYDYAME CHADENTURT LEGTALQARD ITTPEFRIMA WEALHTEG
HITS AT: 159-169, 196-100
    Unspecifical
· . I
    MM
. F.
    CT_{\Lambda}
     UTTO Files: CA, CAPINUS, TOXLIT, USPATFULL
              . PREFERENCES IN FILE CA (1907 T) DATE
               . PEPERENCES IN FILE CASING (1997 TO DATE)
REFERENCE 1: 000:289990
REFERENCE 2: 100:1618 (
126 ANAWER 11 OF 36 PERSISTEN COPYRIGHT 1997 ACC
     175960-67-5 REGISTEN
     Oxidase, lather tercl (Arabidopsis thaliana clame pFL61C1) = 9CI) = (CA
     INLEX NAME
     PROTEIN SEQUENCE
SQL 281
         1 MAADUAYING EVDETSEYNE IVINTHILEAN LWEELEEFIG TWIRNYLAGT
SEQ
        SI LLYTISGERW CEYTYYERIN VYLEKDATET IKANELÇMEV AMRAHEWYTL
       101 LETVORUMIE ROWIRCEASI GEFOWILYFY YLAIYLVETE EGIYWMHERE
       151 HDIKPLYKYL HATHHIYDKO NYLSEFAGLA FHEYDGILOA VPHVIALFIV
                       HOL PIRFOURICE DEMEALWARN THOUSEGNIN PUNGACYRUS HEUTYKENYG
       251 HYTIMINWMF GOLKIPELES DDNRDSFKRA E
HITS AT: 147-151, 161-165, 305-207, 222-326, 239-232, 247-201
115
     Unspecified
CI
     HAN
Sā
LC
     STN Files:
                 CA, CAPLUS, TOXLIT
               1 REFERENCES IN FILE CA (1967 TO DATE)
               1 REFERENCES IN FILE CAPLUS (19.7 TO DATE)
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. PEFERENCE 1: 124:3(30)5
 1.16 ANSWER 12 OF 25 PROJECTRY COPYRIGHT 1990 ACS
 EN 168613-13-6 REGISTEY
  Desaturase, a vylociennyme A (Anacystis midulans strain E2-SPc
      reduced) (9CI) (CA INDEX NAME)
  OTHER MAMES:
  Disaturase, anyl or-mayme A (Symethococour strain PCC 6301)
  FU PROTEIN SEQUENCE
 3QL 278
         1 MTHAIRPKLA PIWPTALEMY AIHIGALLAE LPANEUWPAY GVMVALYYIT
 SEQ
         51 GOFGITLOWH FLISHESFEV EKWLEYYLVE COTLAMINGE IEWIGLHRHH
        101 HERSIGSOON HOSMAGELWS EFLWMIYEIF ARTEVORFTE DIAGDETYEF
        151 FREYFROUDY LLOVILYAWG EAWVONGWSF VVWGIFARLV WYTHYTWLVN
        . 51 GATHEFOTES HEUGDESTNO WWYALLAFGE GWHNNHHAYO YSAFHOLOWW
        US1 EPDLIWINIC COMBUGIARN INVASPIN
 HITS AT: 37-100, 233-2-7
 MF Unspecified
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     MAD
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      CL
      STM Files: CA, CAPLUS
                1 REPERBUCE, IN FILE CA (1967 TO DATE)
                1 REFERENCES IN FILE CAPLUS (1907 TO DATE)
 REFERENCE
            1.16 ANDWER 13 OF THE BEHINDER CONFIGHT 1997 ACC
      163961-98-6 FEGURIFY
 CH
      Decaturace, :atty a dic .omega.6- Arabidopsis thaltana gene fad6)
      (BOI) (CA INDEX MAME)
      PROTEIN SECURIOR
 39L 418
          1 MASSIANCIF AFTGEQQCLE ENPRIAASSA ENVEGYYAVE FIDILLEGET
 SEO
         51 HEREFCUARY KEFIGÜIKAN AARVARPSAD SAEDREQLAE SYGFRÇIGED
        101 GPENYTAKOI MOTEPHENEE HODEKALKSY LITYTOYTIG LEMIAKOPWY
        481 LIPLAWAWIG TAITGEFUIG BUCAHKSESK NELVERIVGT LARLPILTYRY
                                  := = :: ::::=:
        .01 EPWEFFULGER HARTMELMED TAMOPYPEEE FEASPYMRKA LIFGYOPIEP
         31 WEGIAHWIDW HEDLERFFAG EVNEVKISLA CYFAFHAVGW PLEVYRYGIL
         -01 GWYFFWIIGW IGTHEWMOTE TMTHETAPHI PPEPADEWNA AQAQLNGIVH
                                      +51 CDYFEWIEID CHUINWEIPH HISPRIPSYN LEAAHFSIQE NWGKYTNLAT
        401 WINELDETIN TUCHUYDE
 HITS AT: 101-101, 200-11, 325-329, 367-371
 ME.
      Un. pecified
      Matt
      C_{I}
      SHE Files:
                 CA, CALLUS
                  REFERENCES IN FILE CA (1967 TO DATE)
                 I REFERENCES IN FILE CAPLUS (1957 TO DATE).
 EMFERENCE 1: 11:28000
 LL6 ANTWER 14 OF the REGISTRY COPYRIGHT 1997 ACC
      161027-24-3 EEGISTEY
  E.N
      Decaturase, facty acid .DEUTA.15- (Synephocy.tis sp. PCC 6603 clone
      pbluescript/6.u-kbp gene desB] (9CI) (CA INDEX NAME
                            KATHLEEN FULLER BT/LIBEARY 303-4290
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Typ-

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.OTHER NAMES:
    .omoga.? Desaturase (Synechocystis sp. 200 6203 clone
      pRimesoript/6.6-kbp game deser
     GenBank Dulbl?-derived protein GI 1600333
     Pridein (Symethicoyyttis strain PCC 0808 blone
      cal368/mailt: us the "is 0.23% re0391 open roading frame sll1441
      re moed:
      PROTEIN SEASBAIGE
F'. :
     359
\mathbb{F}_{\mathbb{C}}\mathbb{L}
310
          I MELETAGEQT KUPYEKTEEL EFTLQELENA IPAD FEPSV VRSLGYFFLD
         OF TGLIAGPYAL AATDOWPFY DIEWLIGGTL FWOLFTVIGHD CGHISFSKSK
                                                        101 TLMHWIGHLS BTPIAMETHG WRISHRTHHA MTGNIDTDES WYPYSEOKYN
        131 QHANYEKELE FYDPDJAYPI YDFERSYNEÇ GSHFMEGSED FERDEKAAVL
        101 TETFALAREN FELGENINGE ONLENIMERN APPLYEVVMI DIVIELHETE
        161 DULFWYEGDE WYFLEGALST IDEDYGFINE ISHDIGIEVA BELFSIMFRY
        301 KURRATEATK FILGEYYRYS DEPIMQASEK SYWACHEVEN QGSCVYYQSE
        F51 UNGGYQERF
HITS AT: 2 4-94, 1.5-119, 284-292
ME
     Unspection4
· 1
     MAU
Ţ.
     C_{F_{2}}
                  CA, CAPLUS, TOMBLE
PERFERENCES IN FILE CA (1967 TO DATE)
      ETT Files:
                  REFERENCES IN FILE CAPIUS (1907 TO DATE)
REFERENCE 1: 1.7:70 %1
REFERENCE .: 1..1:1.484.
 LU6 ANSWER IS OF BUILDERSTEY COPYRIGHT 1997 ACC
      158651-91-3 FAGISTRY
211
C_{ij}
     Desaturase, farty acid .cmegs.1- (Arabidopsis thalians clone DES1
      CTHEE NAMES:
      Deraturase, :attw-accd .cmeqa.3- (Arabidopsis thaliana gene fad8)
E1.1
      PROTEIN SEMURIME
30L 435
31 Q
          1 MASCULUTECO PERMETENEN HITSEASNER PTENEMERLE ERSSLIMSEN
        11 GPYOPTEIWA LINATELTTL OSPSEEDTEE FORGALEREN LADIRAAIEK
101 HOWMENEWAS INSYLVEIVAL VEGLAAVAAY ENEWLIWELY WEAGGTHEWA
101 DEVISELOGE OFFICIAELIN SVAGELIHUS ILVEYHOWEL SEETHEONEG
        U01 BEENLEAWHE LEEKIYKULE RITOMERETI PERMLAYPRY LWNESPOKQG
        USI CHYHEDCUGE TERREREIMET OTAGWTAMAA LINGINEMMG EIGMIRIYĞI
        301 PYWIFYMWUD FYTYLHHHGH EDKLEWYEGK EWLYLDGGLT TLDEDYGWIN
                              21. fe/ _2:20:00
        301 NORHOOGTHY CHELFTQUPE YHIVEATEAA KPULGHYYRE FKNSGPLPLH
        401 LEGSELEUME JOHFUSDIGD VVYYEADPEL NGORT
HITS AT: 116-16 , 1 1 -19 4, 316-320, 359-363
      Unspecitie:
     MAN
51.
     CA
LC
      STN Files:
                   TILIKOT , BULGAN A:-
                  ARRERENCES IN FILE CA (1 (7 TO DATE)
                5 AMERICANCES IN FILE CAPLUL (1997 TO DATE)
REFERENCE
             1: 125:26:31
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- REFERENCE
             2: 101:007500
 FEFERENCE 3: 121:249101
 LOG ANSWER 16 OF 36 PROJETRY COPYRIGHT 1997 ACS
      158283-34-2 FEGINTRY
     Desaturaso, oleogi moennyme A (master-eil plant clone pRF137C-42
      resuded, 901) OA INDER MAME
 CTHEE NUMBES:
 CII .delta.-11 Fatty +2:0 desaturase (Ricinus communis clone pHF197C-42)
      PROTEIN SEQUENCE
 SOJ
     387
 SEO
          1 MGGOSRMOTY FIGUREERKO OSCHLEFARH TEPRYTEGEL KFAIRPHOFE
          51 KGEMESESNE AYMECLOPLS YSTATNEFFY ISJPLSYVAW LVYWLEQGOI
         101 DIGLWVICHE COHHAEREYQ LADDIVGLIV HSALLVEYFS WKYSHERHHS
         131 NICHLERDEY FYFMSKYMIS WYRKYLNNEP GEWLTLAATL LLGWPLYLAF
        U01 M78988YDAF ACHYDEYGFI FSBEERLQIY IADLGIFATT EVLYQATMAK
        .51 GLAWVMF.LYG VPT.51VNGFL VM.TYLQHTH PATPRYGSSE WDWLRGAMVT
-01 MDF.DYGULNK VPH.NIALCEV AHRLFATVEH YHAMBATKAI KEIMGEYYRY
        -31 DGTEFYHALW REARBOLEVE EDECAPTOGY FWYRNKY
 HITS AT: 1)9-11:, 140-149, 419-32:
 MF Unspecified
      N = 1
 SE.
      \mathbb{C}\mathbb{A}
      STM Files:
                  CA, CALINE
                 1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)
 EMPERENCE 1: 121:.10-40
 L. 6 ANSWER 17 OF 36 REGISTER CORPURIGHT 1997 ACS
      158283-32-0 FEGURTEN
      Desaturase, clecyl boennyme A castor-oil plant clone pFad31
      2.4-amint agia fragment regarded) (PCI) (TA INDEX NAME)
 CTHEF MAMES:
     ..d-lta.-l. Patty and decaturase (Elizanus communis clone pEF2-10)
      PROTEIN SEQUENCE
 301 224
         1 WARAHDOOHH ARVOYQLIDD WVGLILHSCL LVEYESWEHS HERHHENTGS
 Ξ÷Q
                 31 DEFESSIONER FROM IFWYSK YINNPPORIN TIAVTLEDGW FLYLAFNVSG
         101 RPYDEFACHY EDYGFIYNDE ERIBIFISDA GYWAYTEGLY ÇLAIAKGLAW
         181 MYCHYOTELL TOTALFENDIT PLOHTHFALP HYDSSEMDWL EGALATYDED
        101 YGILMEMEHN ITDYQVAHHL ETHE
 HITS AT: 5-9, 41-45
 MF Unspecifica
      MACI
      CA
      STO Files: CA, MANUE
                 1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)
 ERFERENCE
             1: 121:11:046
 1.16 ANIMER 19 OF 96 RESISTEY COPYRIGHT 1997 ACS
      158283-30-8 REGISTRY
      Denaturase, ole-yl coenzyme A (corn blone pFad21 reduced) (9CI) (CA
      INDEX NAME)
 DIHER NAMES:
 CN .delta.-12 fatt; acid desaturase (Zes may; clone pFad2#1)
                              KATHLEEN FULLER BT/LIBFARY 308-4290
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·FS
     PROTEIN SEQUENCE
SQL
     387
          1 MGAGGEMTEK EREKOEOLAR ATGGAAMQES PVEKPPFTLG QIKKAIPPHC
SEQ
         51 FERSYLMOFO YYVHOLUIAW ALLYFALATI PALMSMLKYA AWMLYWIAQG
        101 CUCTONWULA HECORHAFSI YSELDIMYOL VERSEMNEY ESWEYSHERH
                       101 HOUTGSEERD EVENPERKEA EPWYTTYNYN NEUGEDURIU VQLTEGWELY
       101 LATMASGREY PREACHEDRY GRIYMDREFA QIFYSDAGVV AVAFGLYKLA
       . 51 AAS WWWWW. WYAWPLLIWD AMLULITYLQ HTHPSLPRYD SSEWDMLEGA
        -01 LATINELGGI LUBNERNITI THVAHELEST MERYHAMEAT KALEPILGDY
                                    = :::=:=:=:
       49-1 YHEDETEMAK ATWREAGEGI YMEDEDERGM EWYNYKD
HITS AT: 111-111, 14:-111, 331-126
MF
    Ur. pecifica
     MAG
35
     CL
     STN Files:
                  DA, CAELUS
r_{,t}.
                1 REPERENCES IN FILE CA (1967 TO DATE)
                DEFFERENCES IN FINE CARLUS (1967 TO DATE)
            1: 1:1:00:40
REFERENCE
1.6 ANSWER 19 OF 36 AMBISTRY COPYRIGHT 1997 ACS
Γ,
     158283-28-4 F.E.GIRTET
     Desaturase, the ydordersyme A A.Cybean clone pSF2-165F reduced) (201) — CA INDER DAME)
CTHER NAMES:
     .delta.-1. Fasty acid demandrase. Glycine max clone pSF1-165K)
     PROTEIN SEGUENCE
301
    379
          1 MOGROGERARY REQUERTING MENTREPRETV GQLERALPPH CEQESILTER
33.0
        51 SYVVYEQNEA FIFYTATTYF HILEÇEFSLI AWETYWYLQG CLLIGWWYTA
        101 HECCHEAFOF YOMUDDUUGL TIHUTLINEY ESMEISHERH ESMIGALDAD
        191 EMEMEREKSE MAWESEMIND PLOFAMSILM TENDOWERYE AFRYSGREYD
       101 SPASHYHIYA FIYOMERELI IYYOF'ALFS YTYSLYRYAT EKGLYWLLCY
201 YGYPLIIUMG FIYTITYIQH THFALFHYDS SEWDWLEGAL ATMERLYGIL
        301 NEVERHEITET HVAHHLESTE PHYHADEAIN AIPPILGETY GEDOTEFYKA
       FILE INTEMERCIAL MERRICUTER GAZAZENEA
HITS AT: 101-101, 197-141, 911-915
    Unspecified
     MZdI
£F.
     C_{I}
     ETTH Files:
                  CE, CARLUS
(C)
                I PREFERENCES ON PINE CA (1967 TO DAME)
                1 REFERENCES IN FIRE CAPLUS (1907 TO DATE)
EMPERATOR 1: 1.1:.1.64.
5.16 ADDWER 30 OF 46 REGISTRY COPYRIGHT 1997 ACS
     158283-26-2 RECUSTER
EN
V.
     Denaturase, ole yl chemograe A Brassica napus chome pCFN-165D
     rejuded, [901]
                     (CA INDEX NAME)
OTHER NAMES:
CN
     .d-Ita.-12 Facty acts decaturas (Brassic: napus clone pCF2-165D)
     PROTEIN SEQUENCE
F'.3
SQL 383
SEQ
         1 MGAGGENING PESMESETON INRVECETED FT GELERAL PRACTURSIP
         51 RSFSHLIWDI IIASCFYYVA TTYFPLLPNP LSVFAWELYW ACQGOVLTGV
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101 WVIAHECGHA AFSDYDWLED TYGLIFHSEL LYPYFSWYYS HRRHHENTGS
       151 LERDEVEYER RSQUBSGTAS TOTTFGREVN LTUQFTLOWP LYLAFNYSGE
       201 PYTOGGRACHE HEMAPIYNIK ERLÇIYISDA GUNAVOYOLL PYAAVQGVAS
        51 MYOFLEYPLD IYMGELYBIT YLQETHPSLP HYDGSEWIWL EGALATYDED
       FOI YOILNQIFHN ITOTHEAHHL FOTHPHYRAM EATRAINEIL GEYYQFOGTE
       481 MYKAMWREAK ECHYMEPDEQ GERYGVFWYD DELL
HITS AT: 100-100, 141-110, 015-41-
MF
   Un pecified
CI
    MA.:
3 F.
    CI_{\Delta}
     STM File:
                 - CALLUS
               A REFERENCES IN FILE CA (1907 TO DATE)
                1 REFERENCES IN FILE CAPLUS (1 400 TO DATE)
EFFERENCE
            1: 1:1:...6640
196 ANIMER IN OF 36 REGINTEY COPYRIGHT 1907 ACS
    158283-24-0 REGISTRY
    Desaturise, leoyl roombyme A. Arabidophus thaliana clone p92103
    reduced: (+01) JOA INDEX MAME.
FITHER NAMES:
    ..delta.-12 Fitty soid decaturase (Arabidopsis thaliana clone p92103)
    -Olwate desambranc (Arakidopsi) thalisha clone pF2a gene FAD2)
£100
    PROTEIN JEWYFNOL
    383
( __
        1 MCWGGEMENT TUDENSHIET THEMPORKED POMCOLFFAL EPHOFFRSIE
330
        81 RUFSYLISDI ITACCEYYVA THYFSLLEQP DOYLAWCLYW ACQGCYLTCI
       1(1 WITAHE) GRH APCINGWINED TWOLIFHSEN INTERSWAYS BARHREWIGS
       181 DHADEMEVEK ÇADALEWYĞE YEDDELGRIN HUTUÇEVLĞW ELYLAFUVEĞ
       .(1 RPYDOFACHE FEMARIYMER HELÇIYLSDA GILAVOFGLY FYAAAQGMAS
       ASI MICLIFICED DIVAFIVELT TEQUITHPSIP HITTSEWOWL EGALATVORD
       301 YGILLEWERN ITETHVAHEL ESTMEHYNAM BATKAIPPIL GDYYQEDGTP
       751 WYVAMYPEAK ECTYVEPDFE CDFKGYYWYN DEL
HITS AT: 1 0 -1 -, 141-145, 515-11:
7.11
    Unspecifie
Ċ.:
    MED
ĴŦ.
    CF_{i}
     STM Files:
                 CA, CAELUS
               . FEFFENCES IN FIG. (A. 1967 TO DATE)
               . REFFERNORS IN FILE CAPLUS (1 + 7 TC DATE)
EMPERENCE 1: 1.1:.1664*
F.E.E.E.E.M. 'E.
            .d: 1 1:.1435.
106 ANIMER A. OF TO ERCHMINY COPYFIGHT 1947 ACS
     156532-36-4 REGISTEN
    Desaturate, length-outhin (Fyrechoologia strain PCC 7002 gene desA respect (+00) (CA INDEX NAME
DIHER NAMES:
CD Delta 12 desaturase Olymecho to trus PCC7 (...)
F:
     PROTEIN BEQUENCE
SQL 347
         1 HIDVIVEPSA TIMERHPNL ELECTLOTEP ROTYETIPER AWSRVILESVA
SEO
        51 ATTSCYALLA TARWYLLLIV WELTGTTLTG FFTIGHOOGE ESESRESWYN
       101 NLYSHLAFLP LIYPFHSWEI LHNHHHRYTN NMDEDNAWAP FIPELYDDSP
                                  ::====
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151 AFIKAVYRAI RGYLWWLASY IHQLKLHFUW FAFEGEQREQ VRFSALFVII
       201 AGALAFPUME TTUGVWGVVK ENLMEWLGYH EWINSTEILVE HTVPELPFSY
201 EDRWUEATAQ LBUTVHCDYF KWUEVINCHDI NVHVPHHLST GIPSYNLEKA
       301 YASIMQUWGE YLYETKELWE LMMALTEQOH LYGAERNYIS FAGHQKR
HITS AT: \xi = 90, 1.22 - 1.07, 20 - .09
MF
  Unapecitie :
CI
    MAH
SR
    CA
                 MA, MARLUI, TOXLIT
REFERENCES IN FILE CA (1:67 T) DATE
     STN File:
               I REFERENCES IN FILE CAPLUE (1907 TO DATE)
           1: 1. +:2 + 1.7
REFERENCE
REFERENCE 1:1:74°.
106 ANDWER 13 OF 30 REGISTRY COPYRIGHT 1999 ACS
     156532-35-3 REGISTRY
5.11
    Devaturase, - Lebylleouthum (Symechopystis strain POC 6714 gene desA
     reduced: (PCF: (WAIN)EM DAME)
CTHEE NAMES:
In Delta 1. desaturase Symodhopyotis PCC6714)
    ERMEIN CEMUENCE
.3QL 349
        1 MTATIPETER TETSSUPPRE TAICHIQOIT KTIPKECFEK KASHAWASVI.
        51 ITLGATALGY LGCCYLEWYC LEFTWIWTHT ALIGAENWCE DOGERSFAEK
       101 EWYNDEN HI AFAPLIYEFH SWELLHDHHR LRINKSEVEN AMEPWSVEAF
       181 (ASPAIUSIE VERTEGERWW TONIFHWELM HEFLEDEWER DENEVELSIA
       301 VUFLFAAVAF PALLITTOVW GEUREWIMEW LVTHEWMSTF TEVHETIFEI
       FET REPREDENA AMAGINGTUM COMPREVEND CHIONVHIER HISVAIRSYN
       (1 LELAHAMEQ EWSEFLYERT FLWGLMQQUS GOTHLYLPDN GYRTESSLE
HITS AT: (8-9), 118-13., 187-191
MF Unspecified
Ţ. Ţ
    MAH
    (A
                WA, CARLUT, TOXLIT
I REFERENCES IN FILE CA (1:87 T) DATE:
i.c
     STN Files:
                1 REFERENCES IN FILE CAPLUS (1907 TO DATE)
FREEDOM 1: 1/1:74-27
THE ANSWER 14 OF THE REGISTER COPYRIGHT 1980 ACC
     152208-02-1 FEGL: TRY
    Desaturase, firty and torogate- Brassica namus clone FNS gene fad3
    reduced (CI ) A INIER NAME,
CTHER NAMES:
    .cmoga.-2 tatty a mu desaturase. Brassica napus clone END gene fad3)
    PROTÉIN SEQUENCE
3QL 377
         1 MINAMBORIN ANGERFIGG AGEFRIGG FAGGERICKV EURLRINGYV
SEQ
        31 AFFIFATUAL AVAMOTEDSW FEWPLYWAAQ OTLEWALEVL OHLOGHOSES
       101 DIFLENSAUG HIBESPILVE YEGWRISHET ERONEGEVEN DECWVELPER
                                         151 INTENLISHING MILAYTUPLPH LAYPLYLWYR SPOKEGSHYN FYGSLFAPSD
       201 ENLIAT.TTC WSIMLATLVY LUFLVGPVIV LHUYGVHYII EVNWLDAVTY
       251 LHHHGHDARL PWYRGKEWSY LRGGLTTIDE DY HEIMIEH DIGTHVIHHL
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KATHLEEN FULLER BT, LILEARY 308-4290

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331 FPQIPHYHLV DATKSAKHVL GEYYREPKIS GAIPIHLVES LVASIKKDHY
       :51 V.ETGETVEY ETEPELYVYA SEKUKIN
HITS AT: 3. -96, 103-135, 251-256, 195-299
MF Unspecified
    MA::
ĽΙ
110
    CA
     STH Files: CA, CAPLUS, TOXLIT
131
                PEFERENCES IN FILE (A. 1967 TO DATE)
                1 REFERENCES IN FILE CAPLUS (1967 TO DATE)
EFFERENCE 1: 121:47 45
h. 6 ANIWER . E. F. 56 REGISTRY COFFEIGHT 1997 ACS
     152208-01-0 REGISTRY
f-.]]
    Desaturase, :atty acid .omega.3- (Brassida napus chicroplast-encoded
     clane BND seno faul precursor reduced. (BCI) (CA INDEX NAME)
OTHER NAMES:
     ..cmega.-3 tatty abid desaturaso (Brassica napus chloroplast clone
     BMM gene feat precursor)
     PROTĖIN SEJURNOS
.≒. 329
        1 MAYYUEMBAI UFALAAGAAY LNHWLAWPLY WIAQGIMFWA LEVLGHDCGH
.150
        EL GAFRADERIN DUAGHILHSE HIMPYRGWEL SHETHRONEG HYENDESWHP
                                                : ::: :: = :: = :: : : = : = :
       111 MOEKIYEGOD RETREFRETI. PLANILAYPEY LWARSFORKG SHYREDSDLF
131 LEKERNEVIT OTACWTAHAV LLYCLNEVMG PHOMIKLYVI PYWINVMWLD
       101 FTTYLHEHOR EDELPWYRGE EWSTLEGGIT TLDEDYGLIN NUHHDIGTHV
       781 THELEPOTER THIMEATRAA KEVLOKYYEE POKSGEDPLH LUGILAKSIK
       MI EDHFUSIEGD UUYYEADENI YGEIKVTAE
HITS AT: 4\sqrt{-3}, \approx -80, 306-111, 240-263
    Ur.specifie i
     FiZC
. :
     0.7
                  - CA, CARLUS, TOMIT
     STN Files:
                : PEFERENCES IN FILE MA .1967 TO DATE)
: PEFERENCES IN FILE MAPLUS (1967 TO DATE
EFFERENCE 1: 1.1:47048
1.6 MINWER . 6 F H REGISTER COPYRIGHT 1997 ACS
     149956-03-6 EEGISTEN
     Devaturase, fatty arid .DELTA.19- Arabidopsis thaliana clone
     pFack-2 fragment nearced 901 (CA INDEX NAME)
OTHER DAMES:
     .DFLTA.-11cdesaturask frugment Arabidops.s thaliana clone pFadx-2
     plastid
     SPOZEIN SEĞARNGE
. L 156
         1 BUYYKAFTEN WALMVATELT TEQUESEEDR EREDEGAPEP ENLADIFAAI
.15-0
         I PHECWVENEW MUMEYVUEDV AIVEGLAAVA AYENNWILWE LYWFAQGIME
       101 WALFVLGHOC BHGSFSNDPF LNSVAGHLIH SSILVPYHGW RISHETHHQN
                   = := :=
        ISI HGHYEN
HITS AT: 109-112, 144-151
HE
     Unspecified
3:
     MAN
S:.
LC
     STN Files: CA, CAPLUS, TOXLIT
                             KATHLEEN FULLER BT/LIBRARY 308-4290
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REFERENCE

1: 120:47048

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1 REFERENCES IN FILE CA : 1:67 TO DATE)
                1 REFERENCES IN FILE CAPLU: (1967 TO DATE)
             1: 119:153376
FEFERENCE
1.26 ANSWER 37 OF 36 FEGISTRY COPYRIGHT 1947 ACS
     149956-02-5 REGISTEY
     Desaturase, fatty acid .DELTA.15- (corn close pPCE20 fragment
     reduced (901) CA INDEX NAME:
CTHEF MAMES:
CM .DELTA.-15 desaturase fragment (Zea may/ clone pPCR10)
    PROTEIN SEQUENCE
SQL 126
23.0

    1 HHQMHSHIRR DESWHEITER DYRQLEPRIK KLEFT SFFL LAFFVYLLYR

           :=::==::==:::::
        51 SPOKLESHEL ECSDIFSPRE ESDVMUSTTO WOIMLASLLA MACAFGPLQV
       101 LKMYGIEYLV EVNWLDDYTY LEHEGE
HITS AT: 1-P, 122-126
MF Unspecified
     MAN
9.1.
     CF.
     SIN Files: CA, CAPLUS, TOXIII
                1 REFERENCES IN FIGE CA (1967 TO DATE)
                I RESERVOES IN FINE CAPLUT (19-7 TO DATE
F.E.FEF.EN YE
             1: 119:153376
LIG ANSWER 25 OF 50 ESGISTRY COPYRIGHT 1947 ACS
     149956-01-4 REGISTRY
5 M
     Desaturase, fatty soid .DELTA.15- (soyboar clone pSFD-118bwp
     reduced: .301) (CA INDEX MAME)
CIHER MAMES:
    .DELTA.-15 desaturase (Glycine max cuche pSFD-118bwp plastid)
     .cmega.-) fatty arid desaturase [Clycine max chicroplast clone GMD
     gene fadi;
EST
     PROTEIN SEQUENCE
30L 453
       1 MATWYHÇKUG LEGLARVIPE PRIGAALSUT GENERLUTNE VVAGPHEQPL
31 ROMURERNWG LEWSARLEVA SIEEBQKSUT UTUGTUGVEH EHLPRERDPGA
101 PPPPNLADIR AAIPHEONVE DPWRSMSY'U EDVIAUEGLA WAAYLNNWL
BEQ
       181 VWELYWAAQG THEWALFULG HOOGHOSEJI USELNOVVGH LLESSILVEY
                                    =::::::::=::
       201 HGWRISHETH HOHHGHAFNI) ESWHPDPERD FEDLDTVTEN DEFTAPFPLD
                 = := = ::: := :: ::: :=
        381 AFFWYLEGES EGETGSHEDE SSDLEVPNEE EDWITCTACW AAMLGLLVGL
        H(I GEVNGPIQLL KLYGVEYYTE VMWUDLVTYL HEHGHEEKLE WYRGHEWSYL
        351 RGGDTTLORD YGWINNIHRO LGTHVIHHDF PQIPHYHDVE ATEAAKPVFG
       4C1 KYYREPFESA APUPFHLIGE TIESFETDHE 'YSUTGDVVYY QTDSKINGSS
       451 KLE
HITS AT: 171-175, 207-214, G1-335, 374--78
ME'
     Unspecified
C.
     MAN
S:
     CA
LC
     STN Files:
                 CA, CAPLUS, TOXLIT
                2 REFERENCES IN FILE CA (1967 TO DATE)
                2 REFERENCES IN FILE CAPLUS (1947 TO DATE)
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. REFERENCE 2: 119:153.76
 126 ANOWER H9 OF 36 FAGISTRY COPYRIGHT 1997 ACC
      149956-00-3 PEGISTRY
     Desaturase, fatty acid .DELTA.15- sybban chone pXF1 reduced) (9CI)
       (CA INDEX DAME:
 OTHER MAMES:
 \mathbb{C}\mathbb{N}
     .LELTA.-18 desaturase [Glycine max clone pXF1 microsomal]
     .onega.-3 farty acid desaturase (Glyrine max clone GM3 gene fad3)
      FEATEIN DEQUENCE
 SOL
      380
          - 1 MYKUTKELAY AANNGYQOKG SSEDEDESAP PERKIAEIFA SIPKHCWVKN
          11 FWESTSYMBE DVINTAALVA AATHFDHWILL WLTYCPTOGT MFWALFYLGH
         1:1 [CCHRSFORS FLINSINGER] LESSINGER GWEISHFIER QUEGHIERDE
            = 1111112
         151 SWIELTERLY RILLOSMIRLE FETVEFFLEY YELYLESESP GREGSHENRY
         .01 SNDFFFCERK GIADSTIOWA TMFSLNIYLS FITSPLLVIK LYGIPYWIFV
         191 MWOLFWIYLH HHERHQEWPW YEGREWMYLR GGITTYLRIY GWIYNIHHDI
                      = =========
         · 1 OTHVIHHLEP OTERVHIVEA TOAKRYLOD TYREPLESAP LEEHLIKYLI
              : ::: Naisassa
        -04 COMPONERS DISDAVYFOI ISLLIESQED
 EITS AT: 1 = -134, 136-143, 165-265, 366-30
 MF Unspecifies
 0.7
      MAN
      CA
 STM Filed: CA, CAEDUS, TOKLIT
                 . REFERENCES IN FILE CA 1067 TO DATE)

J. REFERENCES IN FILE CAPLUS (1907 TO DATE)
 ERFERENCE 1: 110:47648
 PREFERENCE :: 100:156376
 11.6 ANSWER ROLOF 36 REGISTRY COLYFICHT 1997 ACS
     149955-99-7 REGISTAY
 EII
      Desaturase, fatty acra .DENTA.18- Frassica napus clone pPNSFd-2
      C-terminal transmers requised: (901) CA INDEX MAME
 OTHER NAMES:
     ...DELTA.-15 dlyperplipid desaturase. Frassica napus clone pBNSFd-2
      plantion
      PROTEIN DEQUEIDE
 SUL 404
          1 PMFFQSEMED REFLAMMANIATED TO SEMBEDIESE PRIQREDEGA
 3E.0
         OI PPPENDADIR WAIPEHCAVE DEWESMONIN EELAINEALA AGAAYLINMUL
         1 A AMBIAMANG IMEMANETHS HECCHONETH DEFENDATOR PRESIDENT
         151 HOWELSHEITH HONHGEVEND ESWHPMGERI YEULDRETEF FRETLPHYML
                    .....
        .91 ATPETEMARS PSEKERHYHE DEDLELPKER NOTUTSTACM TAMAVLINCL
        . A DETM SEMEND ELYMTPYWIN MWWLDF TYD HEEGHEDKLP WYRGKEWSYL
                                               . . . . . . . . . . . . . . . .
         301 EGGLTTLDED YGLENNIHHD IGTHVIHHLE PQUPHYHLVE ATEAAKPVLG
                                       ==::::=
         351 EYTEEPDESS PLPLHLIGIL AKSIKEDHEV SDEGDVVYYE ADPNLYGEIK
        401 YTAE
 HITS AT: 121-125, 157-164, 281-285, 324-328
 ME
      Unspecifie t
 C:
      MAN
 SR
 LC
      STN Files: CA, CAPLUS, TOXLIT
                             KATHLEEN FULLER BT/LIBEARY 308-4200
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1 REFERENCES IN FILE (A (1:67 TO DATE)

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1 REFERENCES IN FILE CAPLUT (1967 TO DATE)
          1: 110:153376
REFERENCE
126 ANSWER 31 OF 36 FEGUSTRY COPYRIGHT 1937 ACS
    149955-98-6 REGISTRY
FIL
    Desaturase, fatty and DELTA.15- (Brassida hapus clone pPNSF3-f2
     C-terminal fragment reduced) ( MT1) (CA INDEX NAME)
OTHER NAMES:
    .DELTA.-15 glydered pid desaturase (Brassica napus clone pENSF3-2
    mitrosomali
    FROTEIN SEQUENCE
୍ରପ୍ର 378
         1 LTVIGSSOPP IMMEERITGER DYGAPPPFUL AMIRAAIPKH CWVKNPWKSH
3100
        51 CYMUFELAIM FADAAGANYL MUWLYWPLYW TAQGTHFWAL FVLGHDCGRG
       101 GERMI PELMI AVOHILEGSI IVEYHGWEIS HETHEOMHGH VENDESWEEM
                                            : *:= * ::= ::: ::: =::
      151 PERTYKSIDE PTREFRETIP LYHLAYPFYL WARSPGERGS HYHEDSDLFI
101 PKERNOVETS TARMTANAVL LYGINEVNGP MQMLSTAVIP YWINYMWIDP
       .31 UTYLHEHOHE DRUBWYFORE MOYLEGGLTT LIRDYGDIND IHHDIGIHUD
       FOR HELPEQIETY HIMEATEAAN EVLONYYEEP ORIGELELE LOILAKSIKE
      -31 DHEWSDEGDU WYYEADENIN GEISYTAE
HITS AT: (5-49, 121-12-, 251-.59, 293-0-2
MF Unipedified
0.1
    MAN
£ .
    CL
     STM File: CA, CAPLUE, COXICT
               1 EFFERENCES IN FILE CA (1967 TO DATE)
               1 REFERENCES IN FILE CAPLUD (19:7 TO DATE)
REFERENCE 1: 11 4:1500 6
1..6 ANOWER 31 OF 36 REGISTRY CONVELIGHT 1997 ACM
    149955-97-5 REGISTRY
     Departurase, farty and JEDTA. H- (Arabid pais thalland clone
     pA(F2-, resuced FT) (CA IM(FX NAME)
OTHER DUMES:
    Ci:
    p. :stic:)
     .cnega.-1 fatty act: des durate. Arabidopsis thaliana chloroplast
    clone (FI) generiadi precursor
\mathbb{C}
    ...nega.-0-Fatty act: desiturare Arabidop is thaliana clone g45)
     PROTEIN SEQUENCE
F.
SUL
    446
         1 MANUALSE OF REPLEBLIYET PROMEDSION REFERENCESS YKTSSSELSE
SEO
        51 GLINGEOGETE NEALNUSCEL CTELFEESEL EFINEGEFOR GAPPPENDAD
       101 FRAAIPKEON VEOPWESISY VYRIVAIVFA DÆGGAAYLNI MINWPLYWDA
       151 OGTHEWALEY LORDOOF SEE SIDERLNEWV ORTHRUSTLY PYROWAISHE
                          ----
       201 THEOLEGHTE NORDWERMOR HITTSTLDEFT REFERTIELY MLAYPFYLMA
       351 RSPGEEGOHY HEDODLFLPK ERROVETSTA CWYAMAALDY CLNETIGEIQ
       301 MLELYGIPYW INWMWWDFYT YDHHHGHEDK DFWYE REWS YLEGGLTTID
                                   = 2:= ::=
       351 RDYGLINNIH HDIGTHVIHH LEPPIPHYHL YEATEWAKPY LGKYYKEPDK
       401 SGPLPLHLLE ILAKSIMEDH YUSDEGEV'Y YKUDPNLYGE UKVRAD
HITS AT: 165-167, 199-206, 323-527, 366-370
                           HATHLEEN FULLER BT/LIBEARY 308-4290
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• MF
    Unspecified
CI
     MAN
 ZD.
     \mathbb{C}\Omega
      STN Files: CA, CAPLUS, TCXLIT
                4 PEFERENCES IN FILE CA (1967 TO DATE)
                4 REFERENCES IN FILE CAPLUM (1907 TO DATE)
 PLEEPEIDE
             1: 1.1:297333
            2: 110:184023
 PEFERENCE.
 SEFEREN E
           3: 110:47048
 PEFFENCE
            4: 119:135576
 1.6 AHOWER 33 OF 30 EMGISTRY COPYRIGHT 1997 ACS
      149955-96-4 FEGISTEY
      Devaturase, ratty arid .DELTA.15- (Arabidopsis thaliana clone pCF3
      resuced) (901) (CA INDEX NAME)
 CTHER NAMES:
     .IELTA.-15 desaturase (Arabitopsus thaliana clone pCF3)
      .omega.-3 fatty accd desaturase (Arabidopsis thaliana clone CF3 gene
      fa\cdot (3)
 \Xi^{\prime\prime}
     PROTEIN SEQUENCE
 $QL 386
 EEQ
         - i Myvakojeti vnspegagje kkeerfdra qppfkigjor aaipkhcwyk
         ET SPERCYMYYYY EDITAVAALA TAAVYYDSWF EWFEYWAAQG TEFWAIFVEG
        101 HOGGEGUEDO DECLIMENTOSE ILHEFILVEY HOMFISHETH HOMHGHVEND
            =:::::===
        151 EGWVPLFERN YMELPHSTEM DEYTVPLPHL AYPLYLOYES PGKEGSHENP
        . OI YOSLFARGER ELIMISTICM DINEVGLIAL SEUFGELAVI KVYGVPYIIF
        JEI VHWIDANTYD HHHOHDERDE MYRGKEWSYL EGGDTTIEGD YGIFNNIHHD
        SCI IGTHUIHHIF EQIEHYHIND ATKAAMHVIG RYYREEKTEG AIPIHLVESL
               SEL VASIKKEHYV SOTODIVFYE TOPOLYVYAS DESKIN
 HITS AT: 111-105, 137-144, 161-165, 304-308
     Unspecified
 31.
31.
      MAH
      CL
      STU Files: CA, CARLUS, TOXLLT
. REPERENCES IN FILE CA (1.67 TO DATE)
 LC
                . REPERENCES IN FINE CAPLUS (1987 TO DATE)
 SEFERENCE 1: 101:40648
 FEFERENCE 3: 119:15337+
 126 ALLWER 34 OF SHIPLESTATEY COPYRIGHT 1990 AGS
      148814-49-7 FEGISTER
 F.J
      Dematurase, ratty and d.DELTA.15- (Brassina napus clone pBNDESS gene
      fal3 reduced OCI (CA INDEX NAME)
 OTHER MAMES:
      . mega.3 L.n. hate messturase (Arabi lopsic reduced)
      PROTEIN SEQUENCE
 F3
 SQL 383
          1 MAVAMBARIN VNGOSBARRE EGFDPSAQPP FKIGDIRAAI PKHCWVKSPL
 SEO
         51 RSMSTVTEDI FAVAALAHAA YYFDSWFLWP LYWVAQGTLF WAIFVLGHDC
        101 GHGSFGDIPL LNSTVGHILH SFILVPYH W RIGHRTHHOM HGHVENDESW
            200
        151 VPLPEKLYKN LPHUTEMLKY TVPLFMLAYP IYLWYRSPGK EGSHFNPYSS
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201 LFAPSEPKLI ATSTTCWSIM LATLVYLSFL VDFVTVLKVY GVPYIIFVMW
       251 LDAVTYLHHH GHIEKLPWYF GKEWSYLFOG LUTTERLYGI FMNIHHDIGT
                  ::== ==
       301 HVIHHLEPÇI PHYHLVLATE AAKHVLGEYY REPKTSGAIP IHLVESLVAS
       351 IKEDHYUSET GDIVFYETDE DLYVYASDES KIN
HITS AT: 98-100, 134-141, 158-262, 301-05
     Unsquedified
11F
CIT
     MAH
\Gamma \mathbb{P}
    CL
     STN Files: CA, CARLUS, TOELLT
1.0
               . FEFERENCES IN FILE CA (1:67 TO DATE)
               .. FEFERENCES IN FILE CAPLUT (1967 TO DATE)
FEFEREINE
           1: 121:1973 19
           11: 119:31:629
FF FEFEINGE
10.6 ANGWER 35 OF 6 FEGISTEY COPYRIGHT 1997 ACS
    148734-39-8 FEGISTRY
     Besaturane, lineleate (Tynethocystis strain PCC 6802 clone csy75-3.5
     regreed 1901. COA INDEX MAME
CTHEF MANUES:
    .DELMA. -6-Desaturase (Symeonogystis blone pSyl5-3.5)
\Box \Box
     Desaturase, lineleate (Tymednortis strain PCC 6803)
CT
     GenBank 100014-derived protein 01 160358)
( \cdot , \cdot ]
     Protein Gynech.cystis strain PCC 68 G clone csll23/cettl8-psGll4/cst0681/cst0.94 open reading frame s110262
     reduced:
     PROTEIN SEQUEUCE
.ii_{\cdot}L
    359
        1 MOTABRIMET PREGEREUM JEWOAYFAEH GUTQROMPSM YUKTLIIVUW
. FO
        FI DEPAMARMER ARTIFFORDE GOTOBALADA AFSENVEHDA NENAYSSNEH
                                                      1 1 INFALGMIYO FUGLSSELWE VEHNYLHHOY INGLGHOVET HODGAVEMSP
       191 EGERTSIYRE QQEYIMHLYL FIREYWELYD YYLVLNKGHY HDHKIPPEQP
       301 BELADEL FIR BEWEGYUFGE PLAUSFSIFE VLIGASVOYM TYGIVVCTÎF
       251 MLAHULHOTE ENIPOGESGA IDDEWALCO RITANFATNN PEWNWFCGGL
        301 NHÇVTHHLEP NI HIHTEQL EMILKDYCZE FŞVEYKVYPT FKAAIASNYR
       HOL WIRACISHAS
HITS AT: 88-92, 123-117, 302-300
HF
     Unapecified
7.1
     MAIL
. ! L.
     CA
     STH File: A, CALLUS, TOKELT, USPATFULL
                4 REFERENCES IN FILE MA (1967 TO DATE)
                4 EMPREHIUES IN FELE MAPLUS (1967 TO DATE)
             7: 126:389+6
EEFELENDE
             2: 126:70915
REFERENCE
REFERENCE
             3: 110:154315
REFERENCE
             4: 119:6491:
ER6 ANSWER 36 OF 36 REGISTRY COPYRIGHT 1997 ACS
     131198-85-1 REGISTRY
ECI
     Desaturase, anyl coenzyme A "Saccharomyces cerevisiae reduced) (9CI)
CN
      (CA INDEX NAME)
FS
     PROTEIN SEQUENCE
                            KATHLEEN FULLER BT, LIBRARY 308-4290
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• SQL 510
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1 MPTSGTTIEL IDDQFPKDDS ASSGIVDEVD LITEANILATG LNKKAPRIVN SEQ 51 GFGSLMGSKE MYSVEFDRKG NEKKSNLDEL LEYDNQEKEE AKTKIHISEQ 101 PWTLNNWHOH LNWLNMVLVC GMPHIGWYFA LSGKVPLHLN VFLFSVFYYA 151 VGGUSITAGY HRIWSERSYS AHWPLRLFYA IFOCASVEGS AKWWGHSHEI 201 HHRYTDTLED PYDAREGLWY SHMGWMLLEP NPFYKAFADI TDMYDLWTIR ---251 FQBEHYILLM LLTAFVIPTL ICGYFFNDYM GGLIYAGFIR VFVIQQATEC 301 INSMARYIGT OPFDORATER DIWITALVIR GEGYRNERHE EPTDYRNALK 351 WYQYDPTKVI IYLTSLVGLA YDLKKFSQNA IEHALIÇQEQ KKINKKKAKI 401 NWSPYLTDLP MWDKQTFLAK SKENKGLVII SGIVHDVSGY ISEHFGGETL 451 IKTALGEDAT KAFSGGVYRH SNAAQNVLAD MEUAVIKESK NGAIFMASKE 501 GEIYETCHFF HITS AT: 198-202, 335-339 Unspecified CI MA:I SR STN Files: CA, CAPLUS, TOXLIT LÇ 1 REFERENCES IN FILE CA (1:67 T: DATE)

1 REFERENCES IN FILE CAPLUS (19.7 TO DATE)

REFERENCE 1: 114:18574